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AX406939 Sequence Ax406941 Sequence Ax406947 Sequence AF071002 Homo sapi AF000120 Homo sapi AP0000120 Homo sapi AP0000167 Homo sapi

Description

Run

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Homo agpiens
Bakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Primates; Catarrhini; Hominidae; Homo.
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Polymorphisms associated with cardiac arrythmia
Patent: WO 0222875-A 1 21-MAR-2002;
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Sequence 1 from Patent W00222875.
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AX406939.1 GI:21439814
                                                            SUMMARIES
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AC01842
AL732573
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AX406945
AC096260
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AF046086
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AC10730
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AX406941
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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PAT 14-JUN-2002

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Abbott,G.W., Sesti,F., Splawski,I., Buck M.E., Lehmann,M.H.,
Timchy,K.W., Kasting,M.T. and Goldstein,S.A.
MiRPi forms if Kr potessium channels with HERG and is associated with
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Direct Submission 19719.

Direct Submission Section of Developmental Biology and
Biophysics Department of Pediatrics and Boyer Center for Molecular
Medicine, Vale University School of Medicine, 295 Congress Avenue,
New Haven, CT 06515, UGA.
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/note="mink-related peptide 1, Ala substitued for Thr at anno acid 8"
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Mammalia, Buthoria, Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 732)
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Eukaryote; Wetazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.04; Score 21; DB 6; Length 732;
Best Local Similarity 100.04; Pred. No. 5.8;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      Polymorphisms associated with cardiac arrythmia Patent: WO 0222875-A 9 21-MAR-2002; YALE UNIVERSITY (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/codon_start=1
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Patent: NO 0222875-A 3 21-MAR-2002;
YALE UNIVERSITY (US)
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74. .445
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Mumania Butheria aprimates, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

E. 1 (bases 1 to 100000)

B. Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Homo sapiens genomic DNN, chromosome 21q

I. Published Only in DataBase (1998)

E. 2 (bases 1 to 10000)

E. 2 (bases 1 to 10000)

Discription, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Discription of Science, UST Sequencing Laboratory, Kitasato University,
Squamhara 258, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Teli0427-78-9732, Pax.0427-78-9561)
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                   AP000320 24608 bp DNA linear PRI 20-NOV-1999 Mono sapiens genomic DNA, chromosome 21g22.1, D215226-NML region, clone:01208, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RTKRN), Genomic Sciences Center (GSC); Kiteasco Univ., 1-15-1 Kiteasco, Sagamihara, Kanagawa 228-8555, Mapan (E-main:hattori@gsc.riken.go.jp, 7918-9921, Earsh./App.gsc.riken.go.jp/, 7918-9921,
                                                                                                                                                                         Dikayora' Wetzza, Chordara, Czaniara, Vertebratı, Buceleostomi, Mammala. Butherian Primates, Catarihini, Hominidas, Homo.
In Massa. Butherian Primates, Catarihini, Hominidas, Homo.
Hattoril M. 1846. Toroki, Y. 1946. A. Taylor I. D., Hong-Seog, P., Pulyama, A. 1846. Pool Seog, P., Pulyama, A. 1846. Pool Seog, P., Pulyama, A. 1846. Pool Seog, P., Pulyama, A. 1841. Toroki, Y. 1841. Toroki, Y. 1841. Toroki, Y. 1841. Toroki, Y. and Sakaki, Y. Hong-Seog, P., Pulyama, A. Yada, T. Toroki, Y. and Sakaki, Y. Dy Catarihini Seog, P., Pulyama, A. Yada, T. Toroki, Y. and Sakaki, Y. Dy Catarihini Seog, P., Pulyama, A. Yada, T. Toroki, Y. and Sakaki, Y. Dy Catarihini Seog, P., Pulyama, A. Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequencing project is supported by Japan Science Technology Corporation (4ST) and The Institute of Physical and Chemical Research (RIKEN).
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/organism="Homo Bapiens"
/db_xref="taxon:9606"
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I (Dases I to 809)
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Domenech, A., Estivill, X. and de la Luna, S.
Domenech, A., Estivill, X.
Domenech, A., Estivill, X.
Submitted (01-SEP-2000) Medical and Molecular Genetics Center,
Institut Recerca Oncologica, Avia. de Castelldéfels Km 2,7,
Inspiralet de Llobregat, Barcelona 08907, Spain
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74. .445
/note="potassium channel subunit; MiRP1"
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/db xref="taxon:9606"
/chromosome="21"
/map="21q22"
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens genomic DNA of 21q22.1, GART and AML related, SLC5A3-f4A4
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"Home sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region";
"Dupublished.
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5-3 Worthancho, Chiyoda-Yu, Tokyo 102-1081 Japan Japan
For further information about this sequence, including its
Tocation and relationship to other sequences, please Visit our
sequences archive Web site (intrp://www-alis.tokyo.jsc.go.p.)
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Principal Investigator: Yoshiyaki Sakkri Ph.D.
Principal Investigator: Yoshiyaki Sakkri Ph.D.
sakkaki@ngc.ims.u-tchyo.ac.jp
Sub-lasder: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
Sub-sader: Babanitted by Human Genome Sequencing in ALIS
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                                                                                    100.0%; Score 21; DB 9;
100.0%; Pred. No. 7.7;
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/map="21q22.1"
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Fujiyama, J., Yada, T., Totoki, Y. and Sakaki, Y. Fujiyama, J., Yada, T., Totoki, Y. and Sakaki, Y. CLONE RANGE: B2144714-f5028)

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Hattori, M., Ishli, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y. Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
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Hamo appiens genomic DNA, chromonome 21q22.1, D215226-AML region,
clone 3244F14-F50E0, segment 3/9, complete seguence.
This sequence is conducted by Kitasato University JST sequencing abovatory as a JST sequencing tesm.
Principal Investigator Yoshiyaki Sakaki Ph.D.
Princip 1179=15449-5622, Pax : +81-3-5449-5445,
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/ Organism="Homo sapiens"
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* Keio University School of Medicine, Molecular Biology, * Tokyo
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** Mascheroder Weg 1, D-38124 Braunschweig, Germany, • e.mail:
** Genome@gbf.de
                                  * Institute of Molecular Biotechnology, Genome Analysis, detenbergstrasses 11, D-07745 Jana, Germany, e. e.mail: gscj-submit@genome.imb-jena.de v URL: http://genome.imb-jena.de/
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1 Inhetrase 73 P.14199 Berlin, Germany,

e.mail: info-chr21@molgen.mg.de

WEL http://chr21.rs.berlin.mgg.de/
AL165264: Submitteed (ip-Apr-2000).
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* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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S Hartoria, M. Taylor, T.D., Watanabe, H. Yada, T.,
Parturia, M. Polyyana, A. Taylor, T.D., Watanabe, H. Yada, T.,
Park H.S., Toyoda, A. Taylor, T.D., Watanabe, H. Yada, T.,
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Ponis, M. Taylor, M. Taylor, J. Mannah, M. Schillabal, M. Schuldy, A.,
Sakawasa, S. Shiraral, A. Sakai, T. Wada, J. Shihuya, K. Kawasaki, K. Kawasaki, K. Kawasaki, K. Kawasaki, K. Kawasaki, S. Mannaharia, S. Shiharia, M. Schoel, O. Desairo, A. Rechell, J. Kauer, G. Schaffe, W. Schoel, O. Desairo, A. Rechell, J. Kauer, G. Bolaria, M. Wadar, G. Bolaria, M. Watanaber, K. Kauer, G. Schaffe, W. Wahnaever, S. Borzym, K. Hennigs, S. Rieselamin, L. Degand, F. Lehrach, H., Rainbard, R. and Gardiner, K. Watarcie, P. Lehrach, H., Reinbard, R. and Gardiner, K. Watanaber, R. Barnie, F. Lehrach, H., Reinbard, R. and
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The Chromosome 21 mapping and sequencing consortium consisting of RIKBM Genomic Sciences Center, Human Genome Research Group, .
                                                                41914. .441s7
/hocker.mPMa0866yf9;Genethon Marker;The location is between
each flanking site of PCR primers."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA, chromosome 21q, section 63/105.
AP001719 AL163264 BA000005
AP001719.1 GI:7768719
                                                                                                                                                                                                                                               Sequence 100000 BP; 27731 A; 21990 C; 22220 G; 28059 T; 0 other;
                                                                                                                                                                                                                                                                                                                          100.0%; Score 21; DB 17; Length 100000; 100.0%; Pred. No. 7.7;
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Nature 405 (6784), 311-319 (2000)
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* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                       215 bp mRNA linear MAM 28-SEP-2001 Oryctolagus cuniculus K-/pacemaker channel beta subunit mirpl AF25953 AF27953
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Wymore, R.T., Holnes, B.A., Wymore, R.S., Yu, H., Wu, J., Focapowa, I.,
Zuckerman, J., Pan, Z., Wang, H., Shi, W., Robinson, R., El-Maghrabi, R.
Benjamin, W., Dixon, J.E., McKfinnon, D. and Cohen, I.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoca", Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutherio, Lagomorpha, Leporidae, Oryctolagus.

1. (Dassel t. D. 215)
Yu.H., Wu.J., Potapova, I., Wymore, R.T., Holmes, B., Zuckerman, J., Pan, Z., Mang, H., Shi, M., Robinson, R.B., El-Maghrabi, M.R., Bennjani, W., Robinson, R.B., El-Maghrabi, M.R., Mink-related peptide 1. A beta subuhit for the HCN ion channel subunit family enhances expression and speeds activation 2111149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (IS-DEC-2000) Biology, The University of Tulsa, 600 S. College Av., Tulsa, OK 74104-3189, USA. College Av., Tulsa, OK 74104-3189, USA
                                                                                                            Gaps
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                                                  100.0%; Score 21; DB 9; Length 340000; 100.0%; Pred. No. 8.2;
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/map="21q22.1"
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/note="CpG island"
4272. .4279
/note="NotI site"
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/gene="SLC5A3"
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/procein id="CD153111.1"
/db_xref="G1:214459871"
/fc znn ale idon="MSTLGSPRTOTLEDVFRRIPITYMDN#RONTTAEQEALOAKVDAE
NFYVLIZHAWTGWESETITALLOSTVKSKRREHSNDPYHQYIVEDWGEKYKSQILN
LEESKATTHENIGAAGFOMSP:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/note="The drug associated here was oxatomide."
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Patent: WO 0222875-A 7 21-MAR-2002;
YALE UNIVERSITY (US)
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Pred. No. 39;
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/db_xref="taxon:9606"
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Sequence 7 from Patent W00222875.
AX406945 GI:21439820
       Pred. No.
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       95.2%;
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       Best Local Similarity 95.2
Matches 20; Conservative
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/db_xef="ef1:1911150"
/translation="DAEMPYVUILYLMYMIGMESFIIVAIIJVSTVKSKREHSNDPYH
QYIVEDWQGKYKQQILANEESRATHEBIJGA"
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/bc.vef="Gr.14.9819"
/bc.vef="Gr.14.9819"
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NPYVLLYTVMIGMEGFILVAILVSTVKSKRREHSNDPYHQYIVEDMGEXYKSQILN
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2. (bases 1.0.255)
1.1. // Whore, T. Mitchell, K.E., Wymore, R.S. and Freeman, L.C.
1.1. // Whore, T., Mitchell, K.E., Wymore, R.S. and Freeman, L.C.
Submitted Submission

Veterinary Medicine, Kansas State University, 228 Coles Hall, 1600

Denison Ave., Manhattenn KS 65506-5802, USA
                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthorsia, Cetartiodactyla; Suina; Suidae; Sus.
1 (Dases 1 to 252)
Li, Y., Mitchell, K.E., Wymore, R.S., and Freeman, L.C.
Granulosa cells express multiple KCNQ and KCNE channel subunits (Abstract 1220)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mote-WinK-related peptide 1, Thr substitued for Met at
anno acid 54"
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Sequence 5 from Patent WO0222875.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, David, M. L., Davis, C., Davy-Carrull, L., Dederich, D. M., Douthwaie, K. R., Delgado, O., Denn, A. L., Ding, Y. Dinh, H. H., Douthwaie, K. Y., Draper, H., Dugan-Rocha, S., Durbin, K. J., Barmhart, C., Edgar, D., Edwards, C., Elhal, C., Escorto, M. Falls, F., Garls, A., Ganner, T., Gazza, N., Gill, Gorrell, J. H., Guevara, W. Gunzarne, P., Hale, S., Hamilton, Harris, C., Harris, K., Harr, W. Havlak, P., Hamilton, M. Guevara, W., Gunzarne, P., Hale, S., Hamilton, Harris, C., Harris, K., Harr, W. Havlak, P., Hames, A., Henn Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollinn, Homs, F., Howard, S., Uhber, J., Hollyk, S., Hune, J., Jackboon, B., Jia, Y., Uohnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kally, S., Khan, U., King, L., Korvah, J., Kova, Kratson, E., Kalls, M., Liu, J., Liu, Liu, J., Liu, J., Liu, Liu, J., Liu, Liu, J., Liu, Liu, Liu, Liu, J., Liu, Liu, Liu, Liu, Liu, Liu, Liu, Liu	Maneshwari, M. Mapue P. Martin, R. Martindale, A. Martinez, E., Maneshwari, M. Mapue P. Martin, R. Martindale, A. Martinez, E., Maneshwari, M. Manes, E., Marthofil, T., Mohabbat, K., Morgai, M., Morris, M. Mohabbat, K., Morgai, M., Morris, M., Mo	**C Theses 1 to 117120) Worley.K. Worley.K. Border, Submitseld (17-58P-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Blaza, Houston, TX 77030, USA Action of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Worley.K. Simmitted (11-101200) Human Genetics, Department of Molecular and Muman Genetics, Baylor College of Medicine, One of Molecular and Muman Genetics, Baylor College of Medicine, One	Baylor Plaza, whostcon, Tr 7030, USA  On Jul 10, 2002 this sequence version replaced gi:17943956	* NOTE: Estimated insert size may differ from sequence length (see http://www.hgc.bom.unc.edu/doss/Ghabnk draft data.html).  * NOTE: This is a "working draft' sequence It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of M, but the exact sizes of the gaps are unknown.  * This record will be undated with the finished sequence

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59024 : gapt unknown length
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59025 : gapt unknown length
61015 : gapt of unknown length
61016 : gapt of unknown length
61017 : gapt of unknown length
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92.4%; Scott 19.4; DB 2; Length 117120;
Best Local Similarity 95.2%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps

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Run on:

Seguence:

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Human breast cell single exon nucleic acid probe #8633.
                                                                                                                                                                                                                                                                                                                    Human; microarray; single exon probe;
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                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
31-JAUG-2000; 2000US-06336.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                     ABA49938 standard; DNA; 312
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Human brain expres
Human born marrow
Probe #12706 for gr
Probe #16761 used
Probe #8437 used t
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                             2185239 seqs, 1125999159 residues
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21
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Listing first 45 summaries
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AAK16264
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AAI22773
AAI48075
AAI08446
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ALIGNMENTS

ABA35452

AAS00246 AAC64072 ABA50512 ABA68463 expression; breast;

gene

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Rank

Chen W,

DΚ,

Hanzel

SG,

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Result

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a smalle derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in smaples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging,
                                                                                                                                            measuring human gene expression in a sample derived from human foetal liver. The single acon muclaic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human probe a liver. The present sequence is a single exon nucleic acid human probe of the invention.

Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at firs, wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe #13379 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression; heart; microarray; vascular system; probe; conditionscular disease; hypertension; cardiac arrhythmia; congenituel heart disease; ss.
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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                                                                                                                              The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 22; Length 312; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                Claim 4; SEQ ID NO 16161; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                        Seguence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
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21-SEP-2000; 2000US-0234687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                               The invention relates to a spatially-addressable set of single exon
                                                                                New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
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                                                                                                                                                                                 Claim 4; SEQ ID NO 8633; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foetal liver single exon nucleic acid probe #16161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rom WIPO at ftp.wipo.int/pub/published pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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2000US-0234687.
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                                    WPI; 2001-496933/54
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21-SEP-2000;
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04-OCT-2000;
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monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes with are derived from genomic sequences expressed in the humb brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosts and improved treatment of nervous system diseases such as Althemer's disease, multiple solerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO att ftp.wipo.im/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
apitepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 16255; 650pp + Sequence Listing; English.
                                                                                                                              ö
                                                                                             uuery Match
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches ۱۰ تحما
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 22; Length 312; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe SEQ ID NO: 16255.
                                                                               Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
                                                                                                                                                                   CTCATGTGATGATTGGAATG 124
                                                                                                                                                   1 CTCATGGTGATGATTGGAATG 21
                                                                                                                                                                                                                                  AAK16264 standard; DNA; 312 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207456.
03-UJN-2000; 2000US-068408
03-AUG-2000; 2000US-052346.
21-SEP-2000; 2000US-053359
04-OCT-2000; 2000US-034687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                  (first entry)
                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4PI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  WO200157275-A2
                                                                                                                                                                                                                                                                                 05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                          AAK16264;
                                                                                                                                                                                                                        AAK1626
                                                                                                                                                                                                           RESULT
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leuksemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                    Human bone marrow expressed single exon probe SEQ ID NO: 16565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO: 16565; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                       104 CTCATGGTGATGATTGGAATG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 CTCATGGTGATGATTGGAATG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
1 CTCATGGTGATGATTGGAATG
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                                                                                                                                                               B
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93-UN-2000; 2000US-068408.

03-AUG-2000; 2000US-052346.

21-SEP-2000; 2000US-0234687.

04-OCT-2000; 2000US-0234359.
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                                                                                                                                                               AAK42008 standard; DNA; 312
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                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                 RESULT 5
                                                                                                                                           AAK42008
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Probe #12706 for gene expression analysis in human cervical cell sample.

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Gaps

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0, Indels

0; Mismatches

21; Conservative

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Probe, human, breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nuclaic acid probes (SENP). The proses requerce is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenateal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                     analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID No 16761; 654pp; English
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                                                                                                                                                                                           Chen W, Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCATGGTGATGATTGGAATG 124
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                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
               26-MAY-2000; 2000US-0207456.
30-UN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0523466.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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30-JUN-2000; 2000US-0608408.

21-SEP-2000; 2000US-021366.

21-SEP-2000; 2000US-021359.

04-OCT-2000; 2000US-021459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2001; 2001WO-US00661
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  2000US-0180312
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Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                           Hanzel DK,
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                                                                                                                                                                                                                                WPI; 2001-488897/53
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                                                                                                                                                                                           Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (ESMP). The present sequence is one such probe. The SEMPs are derived from human HeLe colls The SEMPs can be used to produce a single exon successive, which can be used for measuring human gene expression in sample exon human cervical epithelial calls. By measuring one expression, the probes are therefore univil in grading and/or staging one of diseases of the cervix, notably cervical center.

Note: The sequence date for this parent did not form part of the printed specification, but was obtained in electronic forms threatly from Parto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #16761 used to measure gene exprension in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
human; microarray; gene expressinn; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 CTCATGGTGATGATTGGAATG 124
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                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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26-MYY-2000; 2000us-0.201456.

10-JUN-2000; 2000us-0.201466.

10-AMC-2000; 2000us-0.22366.

21-SEP-2000; 2000us-0.234667.

21-SEP-2000; 2000us-0.234665.

04-CCT-2000; 2000us-0.236559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488901/53.
                       cervical cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                               WO200157278-A2
                                                            Homo sapiens.
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                                                                                                                                      09-AUG-2001
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probes, the movel set of probes which hybridisate at high extingency to a probes; the movel set of probes which hybridisate at high extingency to a muchair acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising of a conlection of detecrably labeled microlar acids derived from human lung man, and of lone measuring the label detecrably bound to each probe of the array identifying exons in a entartyotic genome, comprising of the array identifying exons in a entartyotic genome, comprising of the array identifying exons in a less one exon from genomic equences of the entartyote; and (b) detecriby bend to each probe of the entartyote; and (b) detecriby genomic esquences of the entartyote; and (b) detecriby genomic acids from entartyote lung mith, to a single exon probe in included to manufacturing a fragment identical to the predicted exon, the probe is included to comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method comprising (b) identifying exons in several tissues and/or cell types using hybridisation to a single exon in several compression of the exons in the tissues and/or cell types indicates that the exons method exons in the tissues and/or cell types indicates that the exons and the exons in experience of the exons in the tissues and/or cell types indicates that the exons and expenses and exons in the tissues and/or cell types indicates that the exons in experses in the tissues and/or expenses in the tissues and/or expenses and the exons in the tissues and/or expense in th
                                                 The invention relates to a spatially-addressable set of single exon 
the probes for measuring gene expression in a sample derived 
from human lump comprising single exon nucleic acid probes having one of 
12814 nucleic acid sequences mentioned in the specification, or their 
complements or the 1289 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemosiderosis pulmonary histicorytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, faragemer syndrome, fibrocystic pulmonary alveolar proteinosis, faragemer syndrome, fibrocystic and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe #14365 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Robins amount of assistance of assistance of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary diseases (CORD), interstitial lung diseases (LORD), familial didopathic pulmonary fithrosis, naurefithromatoris tuberous sclerosis (Gubb), interstitial aung disease (LORD), familial didopathic pulmonary Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe, human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 24; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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      Claim 4; SEQ ID No 16030; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                  The present invention relates to novel single exon nucleic acid probes. The proses are useful for messuring bunan gene expression in a human breast sample, where the probe hybridises at high extrigency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include breast, cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases and carcinoma tunours.
                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollmonary histicoyrcsis; lymphangiolaiomyomcosis; Karagener syndrome; pulmonary alveolar proteinosis; Ebrocystic pulmonary dysplasia; primary cilary dystinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon probe ORF from lung SEQ ID No 16030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic obstructive pulmonary disease; inčerstitial lung disease;
familial idiopethic pulmonary fibrosis, neurofibromatosis;
tuberous solerosis; daucher's disease; Nieman-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 21; DB 22; Length 312; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyaline membrane disease; open reading frame; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measure gene expression in human lung samples
                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                       Claim 25; SEQ ID No 8437; 322pp; English.
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2000US-236359P.
2000GB-0024263.
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2000US-0608408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
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27-SEP-2000;
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The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast cample, where the probe hybridises at high stringency to a nucleic acid expressed in the human byeast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include breast cancer, disorders of development, inflammatory diseases in the breast, disorders of development, inflammatory diseases of the breast, disorders of development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
angina asthma; disbetes; renal insufficiency; unrary inconfinence
tritleble colon; epilepey; cerebrovascular isofonamia; autofamune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                        non-carcinoma tumours.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                        present invention relates to novel single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel potassium channel gene termed Mink2 encoding potassium channel regulatory protein, useful for screening compounds that are useful for
                                                                                                            Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human potassium channel regulatory protein, Mink2, DNA sequence.
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Pred, No. 1.9;
); Mismatches 0; Indels (
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/product= "MINK2 potassium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                             Claim 25; SEQ ID No 9956; 322pp; English.
                     Rank DR
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                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0379201.
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                     Hanzel DK,
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                                                             WPI; 2001-476286/51.
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                                                                                                                                  in a human breast
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                     Penn
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inflammatory disease, proliferative breust disease, non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human ningle soon nucleic acid probes (SSRP). The present eaquence is one such probe. The SSRPs are derived (SSRP). The present sequence is one such probe. The SSRPs are derived instance of the state of the SSRPs are derived instance of the state of the stat
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                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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100.04; Score 21; DB 22; Length 372;
Best Local Similarity 100.04; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0. Trail
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID No 14365; 487pp; English.
                                                                                                                                                                                                                                                                       Chen W, Rank DR;
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9-UN-2000; 2000US-050408.
03-AUG-2000; 2000US-0523366.
27-SEP-2000; 2000US-0533599.
04-OCT-2000; 2000US-0236399.
                                                             26-NAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-063266.
21-SEP-2000; 2000US-0234687.
   30-JAN-2001; 2001WO-US00670.
                                                                                                                                                       27-SEP-2000; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                  WPI; 2001-488901/53
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                                                                                                                                                                                                                                                                       Penn SG,
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DB 22; Length 450;

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decemining predisposition and/or prognosing beaut disease conse-
expression analysis is useful for assessing the toxicity of chemical
agence ocalls. The microarray of this invention presents a far greater
diversity of probe for measuring gene expression, with far less blus
there age of probes of measuring gene expression is suitable for
rapid approduction of functional information from agenuic sequence. The
present sequence is a single exon muchaic acid probe of the invention
byte: The sequence asks for this patent did not form part of the
princed specification, bour was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, foetal liver, gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample detrived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ttp. wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human foetal liver single exon nucleic acid probe #3557.
                                                                                                                                                                                                            from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                        Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                               Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                     100.0%; Score 21;
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Matches 21; Conserv
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                                                                                      The sequence represents the coding sequence of human potassium channel regulatory protein, Mikz, Bequence is useful for producing a pocassium channel regulatory protein useful for in vitro or in vivo screening of agonistic or antegonistic compounds that are useful for treating of agonistic or antegonistic compounds that are useful for treating diseases caused by aberrant potassium activity, such as human cardiac arrhythmias, hypertension, angina, asthma, diabetes, renal insufficiency, unitary incontinence, riritable ocion, epilepsy, errebackorsecular ischaemia, and autorimment disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled mulcipic acids derived from RNM of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of ragions of genenic RNM predicted to emode proteins. They are useful for yearlying the expression of ragions of genenic RNM predicted to
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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   diseases caused by aberrant potassium activity
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                                            Claim 1; Fig 9; 39pp; English.
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2000US-0234687.
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21-SEP-2000;
27-SEP-2000;
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09-AUG-2001.

ABA44797;

RESULT 13

Query Match Matches

ઠે 요 04-OCT-2000

Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;

Search completed: June 9, 2003, 08:51:25 Job time: 120 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                       Gaps
                                                                                                                                                                                                                                                                                          Probe #3463 for gene expression analysin in human heart cell sample.
                                                                                                                                                                                                                                                                                                                      Human, gene expression, heart; microarray, vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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Score 21; DB 22; Length 450;
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                                       0; Mismatches
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03-UN-2000; 2000US-059408.

03-AUG-2000; 2000US-0523366.

27-SEP-2000; 2000US-034687.

27-SEP-2000; 2000US-034559.
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    Query Match
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GenCore version 5.1.6 .
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES		Match Length DB ID	_	1141 2 US-08-966-316-3 Sequence 3,	9495 1 US-08-271-829-1 Sequence 1,	9495 5 PCT-US93-01544-1 Sequence	19718 4 US-08-961-527-99	836 4 US-08-858-207A-180 Sequence	1569 2 US-08-923-772-1 Sequence	1569 4 US-09-385-287-1 Sequence	2013 4 US-09-423-890-3 Sequence 3,	2465 4 US-09-423-890-9 Sequence 9,	2503 1 US-08-472-934-3 Sequence 3,	2503 1 US-08-472-934-11 Sequence 11,	2503 2 US-08-323-460A-3	2503 2 US-08-461-146C-3 Sequence 3,	2503 2 US-08-461-146C-11 Sequence 11,	2503 3 US-08-461-145C-3 Sequence 3	2503 3 US-08-461-145C-11	2503 4 US-08-628-829-5 Sequence 5	2503 4 US-08-628-829-7 Sequence 7	4729 6 5171684-1 Patent No.	6911 1 US-08-311-174-4 Sequence 4	7577 4 US-08-961-527-46 Sequence 46,	399 4 US-09-641-638-45 Sequence 45,	519 4 US-09-134-001C-1235 Seguence	909 4 US-09-134-001C-334 Sequence 334,	.4 1084 2 US-08-184-009-110 Seguence	
			25002 4	1141 2	9495 1	9495 5	19718 4	836 4	1569 2	1569 4	2013 4	2465 4	2503 1	2503 1	2503 2	2503 2	2503 2	2503 3	2503 3	2503 4	2503 4	4729 6	6911 1	7577 4	399 4	519 4	909 4	1084 2	
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110, App 109, App 109, App 109, App 109, App 11, App 11, App 11, App 11, App 12, App 12, App 12, App 12, App 13, App 13, App 14, App 15, App 16, App 17, App 18, App 1	and Sequences	Gaps 0;	
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S-08-466-736-110 S-06-184-009-109 S-06-184-009-109 S-06-195-110-109 S-06-99-1118-8 S-06-99-1118-8 S-06-99-1118-8 S-06-185-526-8 S-06-185-526-8 S-06-182-1864-9 S-06-11	ALIGNMENTS  27  cus pneumoniae  nces, Inc.  inch, 1.4Mb st.  ion 6.2  1,527  40P1	16.4; No. 89; smatches	
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0 0 0 0 1 0 1 0 1 0 0 0 0 0 1 0 1 0 1 0	RESULT 1 US-08-501  Sequence of Appendix Appendi	Ouery N Best Lo	oy Op

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IDENTIFICATION METHOD:
OTHER INFORMATION: SEG. DIN 0. 5583021 1 is
OTHER INFORMATION: Enc. The CDNA corresponding to the Tobacco OTHER INFORMATION: Etch Virus Genome.
PUBLICATION INFORMATION: ALMOST ALMOST ALMOST ALMOST A.
121 S.W. Salmon Street, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE: TEV propagated in IMMEDIATE SOURCE: N. tabacum Burley 49 POSITION IN GENOME: N/A
                                                                                                                                                            ZIF: 97204

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordParfect 5.1
CURRENT PAPLICATION DATA.
APPLICATION NUMBER: US/08/271,829
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LOCATION: Genomic nucleotides 8518
LOCATION: -9306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Tobacco Etch Virus (TEV)
STRAIN: Highly Aphid Transmitted
                                                                                                                        United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEMONTON DATE: Membrary 19, 1992
CLASSIFONTON: OR DATE: Membrary 19, 1992
ATTORNEY/AGENT INFORMATION:
MANE: MELAN TO STATE TO STATE THE SERVICE TO STATE TO STATE THE STATE TO STATE TO STATE TO STATE THE STATE TO STATE TO STATE THE STATE TO STATE TO STATE THE STATE TO STATE TO STATE TO STATE TO STATE THE STATE TO STATE THE STATE TO STATE TO STATE TO STATE THE STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7942 CTCATGGTCATTATTGCAATG 7962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTCATGGTGATGATTGGAATG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/838,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology
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FRAGMENT TYPE: N/A
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: CD
                                    CITY: Portland
STATE: Oregon
                                                                                          Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE: Sy
JOURNAL:
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PCT-US93-01544-1
                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-271-829-1
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                                                                                                                  Sequence 3, Application Us/08966316
Parent No. 593246
Parent No. 593246
APPLICANT: Lall, Freeti
APPLICANT: All, Freeti
APPLICANT: Murvoung, Janice
APPLICANT: Murvy, Lynn B.
APPLICANT: Murvy Lynn B.
APPLICANT: Mur
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WEDTING TYPE: Distance COMPUTER. IN Compatible
COMPUTER. IN Compatible
SOCTHARD SYSTEM TO Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,316
CLASSIFICATION: 435
PR.OR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/0821829
Patent No. SSBOTA
GENERAL INFORMATION:
APPLICANT: William G. Dougherty and John A.
APPLICANT: Lindbo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Production of Virus
TITLE OF INVENTION: Resistant Plants
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0424 US
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ADDRESSEE: Richard J. Polley
STREET: One World Trade Center
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaci
STREET: 3174 Porter Drive
CITY: Palo Alto
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LENGTH: 1141 base pairs
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Matches 18; Conservative
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STRANDEDNESS: single
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CLONE: 1682433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94304
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US-08-271-829-1
                                          RESULT 2
US-08-966-316-3
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T7.1%; Score 16.2; DB 1; Length 9495;
Best Local Similarity 95.7%; Pred. No. 97;
Matches 18; Conservative 0; Mismatches 3; Indels 0.

Matches 18; Conservative 0; Mismatches 3; Indels 0.
The nucleotide sequence of the Genomic RNA: Evidence for the Synthesis of a Single Polyprotein
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Sequence 99, Application US/08961527
| Patent No. 620135
| CENTEAL INPORMATION:
| CENTEAL INPORMATION:
| APPLICANT: Charles Kunsch
| TITLE OF INVENTION: Strettococcus pneumoniae Polymucleotides and Sequences NUMBER OF SEQUENCES: 391
| CONTESTONDERS 391
| CONTESTONDERS 391
| CONTESTONDERS 391
| CONTESTONDERS 3910 Mest Avenue
| CITY: Rockville
| STATE: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Onery Match
77.1%; Score 16.2; DB 4; Length 1971B;
Best Local Similarity 95.7%; Pred. No. 1.1e.02;
Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER TEACHALL FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER. HP Verset. 486/3.3
COMPUTER. HP VERSET. MSDOS version 6.2
SOFWARM: ASII Text
REPLANTION DATA:
REPLICATION NOMES: 08/08/961,527
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APPLICANT Black, Michael
APPLICANT Knowlee, David
APPLICANT Knowlee, David
APPLICANT: Micholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348128el Compounds
WUMMER OF EQUIENCES, 552
CORRESCENDINGES, 552
CORRESCENDINGES, 552
ADDRESSEE, SALIKHINE Beecham Corporation
STREET, 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 180, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
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                                                                                               7942 CICATGGICATTATTGCAATG 7962
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      1 CTCATGGTGATGATTGGAATG 21
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RECIGTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELERAX: (301) 309-8512
INPORATION FOR ESQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH : 1971B base pairs TYPE: nucleic acid STRANDENNES; double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
                                                                                                                                                                                                                                                                                                     US-08-961-527-99/c
                                                                                                                                                                                                                                                     RESULT 5
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LOANTON: Cost protein gene
LOANTON: Cost protein gene
LOANTON: Cost protein gene
LOANTON: SEC. ID No. 1 is the CDNA
OTHER INPORMATION:
PHIST. CATTON INPORMATION:
Allacoret and allacoret genere of the coding to the TOBACCO Etch Virus Genome.
ATTHER THE PROGRATION:
THE PROGRATION SEC. ID No. 1 is the CDNA
OTHER THE PROGRATION:
THE SEC. IN TO TOBACCO ETCH VIRUS GENOME NAME:
THE STIGNER OF TOBACCO ETCH VIRUS GENOME NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMT: SERSE.

PERJOHENT TYPE.

ORIGINAL SOURCE.

ORGANISM: TODS:

ORGANISM: TODS:

IMBEDIATE SOURCE: TEV Propagated in N. tabacum
IMBEDIATE SOURCE: TEV Propagated in N. tabacum
POSITION IN GENOME: N/A

POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: TBM PC Compatible
CLASSITION NUMBER: PCT/US93/01544
FILING DATE: 19930218
ATTORNEY/ADMINION NUMBER: 18/07/838,509
FILING DATE: 19 FEB 1992
ATTORNEY/ADMINION NUMBER: 28,107
REPERENCE/OCKET NUMBER: 28,107
REPERENCE/OCKET NUMBER: 24,53628/RJP
REPERENCE/OCKET NUMBER: 24,53628/RJP
TELECOMMUTICATION NUMBER: 24,53628/RJP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oregon
: United States of America
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Sequence 1, Application PC/TUS9301544 GENERAL INFORMATION:
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Matches 18; Conservative
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STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: VII
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PAGES: 9-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Oreg
COUNTRY: Un
ZIP: 97204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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Gaps ó

CITY: King of Prussia STATE: PA

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TITLE OF INVENTION! NOVEL (ETH NUMBER OF SECURACES: CORRESPONDENCES: CORRESPONDENCES: ADDRESSE: Decher Price & Rhoads
STREET : 4000 Bell Atlantic Tower, 1717 Arch Stree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.2%; Score 15.8; DB 2; Best Local Similarity 89.5%; Pred. No. 1.2e+02; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DB 4;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GM10080
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09385287
Patent No. 6350857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: «Unknown»
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 rcardardardardar 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 rcanganganggriggaar 298
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STRANDEDNESS: double
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Best Local Similarity 89.5%;
Matches 17; Conservative (
     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
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ZIP: 19103
                                                                                                                                                                                                                         , TOPOLOGY: linear
US-08-923-772-1
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US-09-385-287-1/c
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US-09-423-890-3/c
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Sequence 1, Application US/08923772
GENERAL INFORMATION:
APPLICANT BLACK, Michael T.
TITLE OF INVENTION: NOVEL ##
TUTLE OF INVENTION: NOVEL ##
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
COUNTY AND THE THE THREE FORM:

CONFUTER READABLE FORM:

CONFUTER: IN A COMPAIL DE COUNTY AND THE CONFUTER THE CONFUTER THREE FOR THE CONFUTER THE COUNTY APPLICATION NUMBER: US/08/BS6,207A

FILING DATE: 03-MXY-1997

CLASSIFICATION NUMBER: 06/01500

FILING DATE: 14-MX-1996

ANDER CONFUTER THE CONFUTER TH
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MEDTIME TYPE: Diskette
COMPLITER: INM Compatible
COMPRINES STERM: OF STER
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ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,3354
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TELEPHONE: 215-994-2252
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LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-858-207A-180
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COUNTRY: US
ZIP: 19103
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APPLICATE: JOHNSON, GAPT.
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS NUMBERS OF SEQUENCES. 12
CORRESPONDENCE ADDRESS: ADDRESSES: Labrive and Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GARY L.
METHOD AND PRODUCT FOR REGULATING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTED REACABLE FORM:
MEDIUM TPEE FLORM:
MEDIUM TPEE FLORM:
COMPUTER: LEW PC Compatible
COMPUTER: PE-COSS/MS-DOS
SOFTWARE: PE-COSS/MS-DOS
SOFTWARE: PE-COSS/MS-DOS
APPLICATION NOTA: 1.25
FLUING DATE: OF COSS/MS-DOS
FLUING DAT
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REFERENCE/DOCKET NUMBER: CPI-004DVCP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING BARE: 14-0cc-1994
PROOR APPLICATION BARN:
APPLICATION NUMBER: PCT/US94/11690
FILING BARE: 14-0CT-1994
PRIOR APPLICATION BARN:
APPLICATION MARSER: PCT/US94/04179
FILING BARE: 15-APR-1994
ATTORNEY/AGNY INFORMATION:
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PRICKATION DATA: 308/440,421
APPLICATION NOBERS: 308/440,421
PRICKATION NOBERS: 12.PM2-1995
PRICKATION NOBERS: 308/354,516
PILING DATE: 31.FM2-1995
ROCK APPLICATION NOBERS: 35.405,941
PRICKATION NOBERS: 35.405,941
PRICKATION NOBERS: 35.405,941
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PRICKATION NOBERS: 36.405,941
PRICKATION NOBERS: 308/323,460
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; Sequence 11, Application US/08472934
; Patent No. 575346
; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: U.S.A.
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466..2325
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TITLE OF INVENTION:
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Matches 17; Conserva
                                                                                                                                                                                                                                                                                                        Boston
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                                                                     GENERAL NIPOSMAZIA IN TOTAL CHRONATION GENERAL NIPOSMAZIA IN TOTAL CHRONATION GENERAL STATEMATON GENERAL CORPORATION IN THE GENERAL GENERAL CORPORATION INCLEIC ACID MOLECULES TILLS OF INVENTION IN THE SERVICE TO THE 
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Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.2%; Score 15.8; DB 4; Length 2465; 89.5%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels 0;
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Patent No. 6312934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           951 CTCCTGGTGATGATAGGAA 933
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Patent No. 5753446
Sequence 3, Application US/09423890
Patent No. 6312934
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Matches 17; Conservative
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; LOCATION: (124)..(1980)
US-09-423-890-3
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US-09-423-890-9
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ORGANISM: Homo sapiens
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US-08-472-934-3/c
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LENGTH: 2465
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UGS-05-461-146C-3/A

1 Sequence 3, Application US/00461146C

1 Sequence 10. SPB165

1 SERIAL INCRMATION:
GREENL INCRMATION:
GRE
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WIGHTON THEE FROEDPY disk
COMPUTER: IN THE FROEDPY disk
APPLICATION NUMBER: US 08/049,254
TELECROMONICATION NUMBER: 28/90-1-1
TELECROMONICATION NO 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE Datemtin Release #1.0, Version #1.25 CURRENT PAPLICATION DATA.
APPLICATION NUMBER: US/08/461,146C
FILING DATE: 05-5-UN-1995
CLASSIFICATION: 435
RACE PALICATION NATA.
APPLICATION NUMBER: US 08/354,516
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Best Local Similarity 89.54; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismarches
                                                                                STREET: 1700 LINCOLN STREET, SUITE 3500 CITY: DENVER
                                           SHERIDAN ROSS & MCINTOSH
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ADDRESSEE: Lahive and Cockfield
STREET: 60 State Street
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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; LOCATION: 466..2325
US-08-323-460A-3
      CORRESPONDENCE ADDRESS
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ZIP: 80203
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US-06-322-460A-3/C
US-06-322-460A-3/C
US-06-322-460A-3/C
SEQUENCE A. INFORMATION OF SEGUENCE
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING CELL
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS
NUMBER OF SEQUENCES: 10
TITLE OF INVENTION: RESPONSIVENESS TO EXTERNAL SIGNALS NOMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MURCHINA TREE: ROOPE disk

COMPUTED: INF PC compatible

COMPATION

CLASS FROTATION

FILING DATE: 1956

FILING DATE: 1967

FILING DA
                                                                                                                           E: Lahive and Cockfield
60 State Street
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy
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LOCATION: 466
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                                                                                                                                       ADDRESSEE:
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Parent No. 59151701.
APPLICANT. JOHNSON, GARY L.
APPLICANT. JOHNSON, GARY L.
APPLICANT. OF INVENTION: WERHODS FOR REGULATING MEXX PROTEIN ACTIVITY NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Labive and Cockfield
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT PAPLICATION DATA: APPLICATION NUMBER: 08/08/461,146C FILING DATE: 08/08/461,146C CLASSIFICATION: 435
PRIOR APPLICATION DATA.

PRIOR APPLICATION DATA.

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PLING DATE:

PRIOR PRIOR WHORE R.

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APPLICATION NOMBER: US 08/354,516
FILING DATE: 21.FEB.1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/049,254
FILING DATE: 12-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/323,460
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MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 227-5941
INPORATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2503 base pairs
TYPE: nucleic acid
STRANDENNESS: double
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
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; LOCATION: 466..2325
US-08-461-146C-3
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MOLECULE TYPE: CDNA
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PRIOR DATE: 14-0CT-1994
PRIOR APPLICATION DATA: 0CT-1994
PRIOR APPLICATION MARBER: 0CT/US94/11690
PRIOR PREDACTION MARBER: 0CT/US94/11690
PRIOR PREDACTION DATE: 1994
ATTORINY AGAIN THEOMATION: NORINY AGAIN THEOMATION: NORINY AGAIN THEOMATION: NORINY MARBER TO TELECHOMATION: TELECHOMATION OF TELECHOMATICS OF TELECHO
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STRANDEDNESS: double
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; LOCATION:
US-08-461-146C-11
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9, 2003, 09:12:21; Search time 59.5 Seconds (Without alignmenta) 499.594 Million cell updates/sec
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1. /cgn2_6/prodata/l/pubpna/PCT_NBW_PUB.seq:*

2. /cgn2_6/prodata/l/pubpna/PCT_NBW_PUB.seq:*

3. /cgn2_6/prodata/l/pubpna/NCG6_NBW_PUB.seq:*

4. /cgn2_6/prodata/l/pubpna/NCG6_NBW_PUB.seq:*

5. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

6. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

7. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

8. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

9. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

9. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

10. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

11. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

12. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

13. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*

14. /cgn2_6/prodata/l/pubpna/NCGG_NBW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870385 seqs, 699768693 residues
                                                                                                                                                                                                                                                                               US-09-550-163-1_COPY_230_250_21
1 ctcatggtgatgattggaatg 21
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Maximum Match 100%
Listing Eirst 45 summaries
                                                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Pred. No. is the number of results predicted by chance to have a sorre greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	Ouery Match	Query Match Length DB	DB	ID	Description
-	21	100.0	312	10	US-09-864-761-20233	Sequence 20233, A
8	21	100.0	372	10	US-09-864-761-33139	Sequence 33139, A
m	21	100.0	450	10	US-09-864-761-3463	Sequence 3463, Ap
4	21	100.0	471	10	US-09-864-761-16671	Sequence 16671, A
S	21	100.0	732	σ	US-10-000-151B-5	Sequence 5, Appli
9	21	100.0	113604	6	US-10-227-195A-1	Sequence 1, Appli
7	21	100.0	113604	σ	US-10-227-195A-2	
80	16.8	80.0	583	10	US-09-864-761-20772	Seguence 20772. A
σ	16.8	80.0	707	6	US-10-011-585A-78	Sequence 78, Appl
10	16.8	80.0	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 11	16.4	78.1	1350		US-09-769-787-322	Sequence 322, App
12	16.4	78.1	1448	6	US-09-774-639-63	Sequence 63, Appl
13	16.4	78.1	1448	φ	US-09-969-730-52	Sequence 52, Appl
c 14	16.2	77.1	227	10	US-09-294-093B-5363	Sequence 5363, Ap
15	16.2	77.1	481	6	US-09-968-433-26	Sequence 26, Appl
c 16	16.2	77.1	574	10	US-09-864-761-12791	Sequence 12791, A
17	16.2	77.1	1141	6	US-09-968-433-3	Sequence 3, Appli
18	16.2	77.1	1653	10	US-09-529-063-80	Sequence 80, Appl
19	16.2	77.1	2000	10	US-09-529-063-81	Sequence 81, Appl

Sequence 10, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7121, Ap	Sequence 3431, Ap Sequence 898, App Sequence 314, App Sequence 2905, Ap Sequence 2427, Ap	Sequence 300, App. Sequence 1, Appli Sequence 9156, Ap Sequence 75, Appli Sequence 3, Appli	Sequence 55, Appli Sequence 55, Appl Sequence 11, Appli Sequence 4825, Ap Sequence 17878, A Sequence 6564, Ap Sequence 29571, A	Sequence 6372, Ap Sequence 53, Appl Sequence 106, App Sequence 3002, Ap
US-09-956-712-10 US-09-939-964-1 US-09-790-988-1 US-09-878-574-7121 US-09-878-574-7121	US-09-878-574-3431 US-09-770-445-898 US-09-822-846-314 US-09-738-626-2905 US-09-815-242-9427	US-09-938-842A-300 US-09-814-041A-1 US-09-815-242-9156 US-09-981-353-75 US-10-000-864-3	2 US-00-864-9 US-09-801-368-55 US-09-9138-626-1 US-09-938-8423-4825 US-09-864-761-17878 US-09-966-352-6504 US-09-864-761-29571	US-09-878-574-6372 US-09-782-974C-53 US-09-984-130-106 US-09-878-574-3002
96649 9 536165 9 640681 10 257 10	382 774 774 1029 1395	1524 1569 1672 1672 1675 2013	2465 12 6504 10 3309400 9 2000 9 109 10 167 10	260 10 335 9 340 9
77.1	75.2	75.2 75.2 75.2 75.2	2.25.2 2.25.2 2.25.2 4.25.4	72.4 72.4 72.4 4.27
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ALIGNMENTS

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US-9-9-94-71-1463

Degenance 1463, Application US/09864761

PROTECT NO. US2000004487631

PROTECT NO. US2000004487631

APPLICANT: Hank, David R.
APPLICANT: Hank, David R.
APPLICANT: CHARLE DAVID SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: HERNANGENORM DERIVED SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: HERNANGENORM DAVID SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: HERNANGENORM DAVID SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: HERNANGENORM DAVID SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION WINDERS 10/19/964.761

PRIOR FILENCE DAVID SINGLE DAVID SINGLE EXON NUCLEIC ACID PROBES USBFUL FOR THE PRILATION NUMBER 10/19/964.761

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PRIOR FILENCE DAVID SINGLE DAV
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OTHER INFORMATION: EXRESSED IN HELLA, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELLO0, SIGNAL = 0.67
OTHER INFORMATION: EST HUMAN HTT: ALGS4552.1, EVALUE 0.000
OTHER INFORMATION: ST SERVEN HTT: QY84.05, EVALUE 8.000-67
OTHER INFORMATION: SHISSPROT HTT: QY84.05, EVALUE 8.000-67
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRICOR PULICATION DATE: 2001.01.30

PRICOR APPLICATION NUMBER: PCT/USO1/00668

PRICOR APPLICATION NUMBER: PCT/USO1/00663

PRICOR APPLICATION NUMBER: PCT/USO1/00663

PRICOR APPLICATION NUMBER: PCT/USO1/00663

PRICOR APPLICATION NUMBER: PCT/USO1/00663

PRICOR PLIANCE 2001.01.30

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ORGANISM: Homo sapiens
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GENERAL INCOMENTION:
PAULICANT: Rain, David R.
APDLICANT: Rain, DAVID RAIN
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OTHER INFORMATION: MAP TO APD00052.1
OTHER INFORMATION: EXPRESSED IN BOUN WARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HIGHLOW, GIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HIGHLOW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HIGH, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HIGH, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN HIGH, SIGNAL = 0.9
OTHER INFORMATION: STREESSED IN HIT: AT246.29-1, EVALUE 0.00e+C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 20233.
       PRICOR APPLICATION WURBER: PCT/USO1/00670
PRICOR PRICATION DATE: 2001-01-10
PRICOR APPLICATION WURBER: US 60/234,687
PRICOR PRICORTION WURBER: US 60/246,687
PRICOR PRICORTION WURBER: US 69/608,408
PRICOR APPLICATION WURBER: US 69/774,203
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PRIOR APPLICATION UNMERS: PCT/US01/00669
PRIOR FLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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Patent No. US20020048763A1
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APPLICANT: Balser, Jeffrey R. APPLICANT: Balser, Jeffrey R. APPLICANT: George, Alfred L. TITLE OF INVENTION HIGHAR KCR. REGULATION OF HERG POTASSIUM CHANNEL BLOCK FILE REPRENDENT: Vanderblik Ref. No. US20030013136A1 VU0120; Attorney Docket No. US200 CURRENT FILING DATE: 2000-10-30 CURRENT FILING DATE: 2000-10-30 SOFTWARE: PALENTIN NOS: 5 SOFTWARE: PALENTIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%; Score 21; DB 10; Length 471;
Begt Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels (
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 0.67
US-09-864-761-16671
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SEQ ID NO 16671
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                                                                                                    FRIOR APPLICATION NUMBER: PCT/USO1/0664

REIGR PLICATION NUMBER: PCT/USO1/0669

REIGR PLICATION NUMBER: BCT/USO1/0669

REIGR PLICATION NUMBER: US 09/609,408

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RUMBER: PLICATION NUMBER: US 09/609,408
                     APPLICATION NUMBER: PCT/US01/00667
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 21; Conserv
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| ARRIAL INCORPARATION:
| APPLICANT: Feat, David R. |
| APPLICANT: Feat, David R. |
| APPLICANT: Hanzel, David R. |
| APPLICANT: HANSEL |
| TITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVERTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE OF INVERTION: ONLOGER: US / 09/864,761 |
| CURRENT FILING DATE: 2001-05-20 |
| PRIOR PLILATION NUMBER: US 60/180,312 |
| PRIOR FILING DATE: 2000-06-20 |
| PRIOR FILING DATE: 2000-06-20 |
| PRIOR PLILATION NUMBER: US 69/532,46 |
| PRIOR PLILATION NUMBER: US 69/236,359 |
| PRIOR PLILATION NUMBER: US 60/236,359 |
| PRIOR PLILATION NUMBER: PET/USO1-01-30 |
| PRIOR PLILATION NUMBER: PET/USO1/00666 |
| PRIOR FILING DATE: 2000-09-27 |
| PRIOR PRILATION NUMBER: PET/USO1/00666 |
| PRIOR PRILATION NUMBER: PET/USO1/00666 |
| PRIOR PRILATION NUMBER: PET/USO1/00666 |
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OCTER INCOMPATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OCTER INCOMPATION: EXPRESSED IN HBLIOO, SIGNAL = 1.1

OCHER INCOMPATION: EXPRESSED IN MOLI LURE, SIGNAL = 1.3

OTHER INCOMPATION: EXPRESSED IN HBLAIK, SIGNAL = 1.4

OTHER INCOMPATION: EXPRESSED IN PLACENTY, SIGNAL = 1.4

OTHER INCOMPATION: EXPRESSED IN PLACENTY, SIGNAL = 1.4

OTHER INCOMPATION: EXPRESSED IN HEAL LURE, SIGNAL = 1.4

OTHER INCOMPATION: EXPRESSED IN HEAL SIGNAL = 0.94

OTHER INCOMPATION: EXPRESSED IN HEAL SIGNAL = 0.94

OTHER INCOMPATION: EXPRESSED IN HEAL SIGNAL = 0.94

OTHER INCOMPATION: EXPRESSED IN HEAL SIGNAL = 0.98
PRIOR APPLICATION WUMBER: PCT/USO1/00665
PRIOR FILING DADE: 2001-01:30
PRIOR FILING DADE: 2001-01:30
PRIOR PLILING DADE: 2000-09:21
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PRIOR PLILING DATE: 200
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ORGANISM: Homo sapiens
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INFORMATION EXPRESSED IN HELLO SIGNAL = 2.3
INFORMATION EXPRESSED IN PLACENTA SIGNAL = 2.4
INFORMATION EXPRESSED IN PLACENTA SIGNAL = 2.4
INFORMATION EXPRESSED IN PRIAL LIVER, SIGNAL = 2.4
INFORMATION EXPRESSED IN REPRAIL LIVER, SIGNAL = 2.7
INFORMATION EXPRESSED IN REPRAIL SIGNAL = 2.7
INFORMATION EXPRESSED IN HARROW SIGNAL = 2.7
INFORMATION EXPRESSED IN HARROW SIGNAL = 2.7
INFORMATION STREESSED IN HARROW SIGNAL = 2.7
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REIGNE APPLICATION UNDERS. 105 -0.5 -3.

PRICE FILING DATE: 2000-0.2 -4.

PRICE FILING DATE: 2000-0.3 -4.

PRICE FILING DATE: 2001-0.4 -4.

PRICE FILING DATE: 2001-0.4 -4.

PRICE FILING DATE: 2001-0.3 -4.

PRICE PRICE TOTION UNDERS: PCT/USO1/00665

PRICE FILING DATE: 2001-0.3 -4.

PRICE PRICE TOTION UNDERS: 2001-0.3 -4.

PRICE PRICE TOTION UNDERS: CPT/USO1/0067

PRICE FILING DATE: 2001-0.3 -4.

PRICE PRICE TOTION UNDERS: PCT/USO1/0067

PRICE FILING DATE: 2001-0.3 -4.

PRICE APPLICATION UNDERS: US 99/608,408

PRICE PRICE ZOND: 2001-0.3 -4.

PRICE ZOND
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ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION:
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SEQ ID NO 20772
LENGTH: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-011-585A-78
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Petern No. US200200476331

GRBEAL INCORMATION: Farm. Sharron G.

APPLICANT: Farm. Sharron G.

APPLICANT: RATE. David K.

APPLICANT: HARREL David K.

APPLICANT: HARREL DAVID K.

APPLICANT: HARREL DAVID K.

APPLICANT: HARREL DAVID K.

APPLICANT: TITLE OF INVENTION: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GREE EXPRESSION ANALYBIS BY MICKOARRAY

CURRENT APPLICATION NOWERS: US/09/864,761

CURRENT APPLICATION NOWERS: US/09/864,761
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Best Local Similarity 100.0%; Pred. No. 4.6;
Best Local Similarity 100.0%; Pred. No. 4.6;
Asches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 21; DB 9; Length 113604; Best Local Similarity 100.0%; Pred. No. 4.6; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US/20030077633A1
GENERAL INFORMATION
APPLICANT Cox, David
APPLICANT Tox, David
APPLICANT Tox, David
APPLICANT TOX, David
APPLICANT TOX, David
APPLICANT NOW Haplocype structure of chromosome 21
FITLE REFERENCE: 103 001
COMMENT PRILIAGO NUMBER: US/10/227,195A
COMMENT FILING DAVE: 2003-11-18
NUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 3
SEQ ID NOS: 3
SEQ ID NOS: 3
SEQ ID NOS: 4
                                                                                                                                                                                                                          APPLICANT: Arnold Deana
TITLE OF INVENTION: Haplotype structure of chromosome 21
TITLE OF INVENTION: Haplotype structure of chromosome 21
TITLE OF INVENTION: Haplotype structure of chromosome 21
CURRENT PELIAGO MATE: 2002-11-18
SOFTWART FILLING DATE: 2002-11-18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1715_ 7204, 36973, 66372, 76921, 81512, 88727
OTHER INFORMATION: n = G or C
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                                                                                             Sequence 1, Application US/10227195A Publication No. US20030077633A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
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                                                        -10-227-195A-1
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OTHER INFORMATION: MAP TO AL022334.1

OTHER INFORMATION: EXPRESSED IN BT74, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BTAIN, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN HALLO, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN PLACENYA, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN PLACENYA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN FULL LIVER, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN FOULT LIVER, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN FOULT LIVER, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN FOULT LIVER, SIGNAL = 2.7
                                               630 CTCATGGTGAAGATAGGAAT 649
                       1 CTCATGGTGATGATTGGAAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Recipon, Herve
APPLICANT: Chen, 561-Yu
APPLICANT: Liu, Chensis, 101-Yu
APPLICANT: DR. 2005-11-14
CURRENT FILING DATE: 2005-20-14
PRIOR APPLICATION WHORRE: 60/244, 740
PRIOR APPLICATION WHORRE: 60/244, 740
NUMBER OF 800 ID NO: 2.15
SSO ID NO: 2.45
SSO ID NO: 2.45
LENGTH: 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 16.8; DB 9; Length 707; 90.0%; Pred. No. 1.9e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                  MAME/KEY: unsure
MAME/KEY: unsure
COTHER INFORMATION: a, c, g or t
NAME/KEY: unsure
COTHER INFORMATION: a, c, g or t
NAME/KEY: unsure
LOCATION: (1859)
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OTHER INFORMATION: a, c, g or t
NAME/KEY: unsure
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; OTHER INFORMATION: a, c, g or t
US-10-011-585A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (436)
OCTHER INFORMATION: a, c, g or NAME/KEY: unsure
LOCATION: (477)
OTHER INFORMATION: a, c, g or
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OTHER INFORMATION: a, c, g or
RAME/KEY: unsure
LOCATION: (521)
OTHER INFORMATION: a, c, g or
NAME/KEY: unsure
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OTHER INFORMATION: a, c, g or
NAME/KEY unsure
LOCATION: (561)
OTHER INFORMATION: a, c, g or
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OTHER INPORANTION a, c, g on
NAME/KEY: UNBLYE
LOCATION: (679)
OTHER INFORMATION: a, c, g on
NAME/KEY: UNBLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (434)
OTHER INFORMATION: a, c, g
NAME/KEY: ungure
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Best Local Similarity 90.0
Matches 18; Conservative
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LOCATION: (482)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: a,
NAME/KEY: ungure
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LOCATION: (583)
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Sequence 52, Application US/09969730

Publication No. US20030054443A1

GREEKL INFORMATION:

Publication No. US20030054443A1

APPLICATION No. US20030054443A1

TITLE REPRENCE: POLITY

FILE REPRENCE: POLITY

CURRENT FILING DATE: 2001-10-04

FRICH APPLICATION NUMBER: US/09/69,730

CURRENT FILING DATE: 2001-10-04

PRIOR PLILON ON NUMBER: US/074,639

PRIOR PLILON GATE: 2001-10-04

PRIOR PLILON GATE: 2001-10-04

PRIOR PLILON DATE: 1999-00-04

PRIOR PLILON MUMBER: US/074,112

PRIOR PLILON NUMBER: US/024,112

PRIOR PLILON DATE: 1999-00-04

PRIOR PLILON DATE: 1999-00-04

PRIOR PLILON DATE: 1999-00-04

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON NUMBER: 60/056,371

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON NUMBER: 60/056,374

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON NUMBER: 60/056,364

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON APPLICATION NUMBER: 60/056,371

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON APPLICATION NUMBER: 60/056,301

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON NUMBER: 60/054,806

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 1997-08-19

PRIOR PLILON DATE: 60/054,806

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PRIOR PLILON DATE: 60/054,806

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PRIOR PLILON DATE: 1997-08-19

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SOFTWARE: PatentIn Ver. 2
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ORGANISM: Homo sapiens
                                                                US-09-969-730-52
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TITLE OF INVENTION: 90 Human Secreted Proteins
TITLE OF INVENTION: 90 Human Secreted Proteins
TITLE OF INVENTION: 90 Human Secreted Proteins
CURRENT PROLICATION WINNERS: 105/05/09
PRIOR APPLICATION WINNER: EARLIER APPLICATION WINNER: 09/244,112
PRIOR APPLICATION WINNER: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SEQ TION 00 63
                                                                                                Length 1959;
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Best Local Similarity 94.4%; Pred. No. 3.38-02.
Best Local Similarity 94.4%; Pred. No. 3.38-02.
Matches 17; Conservative 0; Mismatches 1, Indels 0
Matches 17; Conservative 0; Mismatches 1, Indels 0
                                                                                                                                                    Indels
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
US-09-864-761-4012
                                                                                        Query Match 80.0%; Score 16.8; DB 10; Best Local Similarity 90.0%; Pred. No. 3.2e+02; Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Microtial Technice Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Ranabro, Philip M
TITLE OF INVENTION: Processing
FILE REPERENCE: PMC/P21129W0
CURRENT APPLICATION WUMBER: US 00/97769,787
CURRENT FILINO DATE: 2001-01-26
PRIOR FILING DATE: 1309-01-17
PRIOR FILING DATE: 1399-03-17
PRIOR APPLICATION NUMBER: US 60125164
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 322, Application US/09769787
Publication No. US20030091577A1
GENERAL INFORMATION:
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Publication No. US20030003555A1
GENERAL INFORMATION:
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; ORGANISM: Streptococcus pneumoniae
US-09-769-787-322
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SEQ ID NO 322
LENGTH: 1350
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ORGANISM: Homo sapiens
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US-09-769-787-322/c
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Query Match 77.1%; Score 16.2; DB 9; Length 491; Best Local Similarity 95.7%; Pred. No. 3.5e+02. Matches 18; Conservative 0; Mismatches 3; Indels (
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Fatern No. USZ010/005135A1

GENERAL INFORMATION:
APPLICANT:
Lolagudi, Raghunath, V.
APPLICANT:
APPLICANT:
Lolagudi, Raghunath, V.
APPLICANT:
APPLI
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                                                                                                                        Query Match 78.1%; Score 16.4; DB 9; Length 1448; Beet Local Similarity 94.4%; Pred. No. 3.38+02. Marches 17; Conservative 0; Mismatches 1; Indels 0
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700356460H1
NAME/KEY: unaure
LOCATION: 195, 206
OTHER INFORMATION: a, t, c, g, or other
US-09-298-0918-358-3
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OTHER INFORMATION: Incyte ID No. US20030073162A1 2444714F6
UG-0-686433-26
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Publication No. USZ0030073162A1

Publication No. USZ0030073162A1

APPLICANT: Lal. Preeti

APPLICANT: Lal. Preeti

APPLICANT: Marky, Lynn E.

APPLICANT: Reddy, Roopa

APPLICANT: Marky, Lynn E.

APPLIC
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H95139 yw59C08.s1 BG221966 RST41783 BG14301 602286063 BQ526572 NISC no17 BH872665 hp07e09.b

T18753 2C02A04-T7 BQ3333632 WR4-PT005 AQ482802 RPCI-11-2 BJ269854 BJ269854 AA76105 NY13d09.s BF754132 CAA-CT051 BG931453 f33-88

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Run on:

Sequence:

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Homo sapiens

Bukaryota, Wetazoa; Chordata; Craniata; Verrebrata; Buteleostomi;

Bukaryota, Wetazoa; Chordata; Craniata; Verrebrata; Buteleostomi;

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),

Umpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Ggapber-remail: nih; goo.

Tissue Producement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmett-Buck, M.D., Ph.D.

CONTA Library Preparation: M. Bento Soares, Ph.D.

CONTA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Close distribution: WGI-GGAP close distribution information can be found through the I. M.A.G. & Consortium/LLML at:

www.bb.llnl.sov/bbrplinage/image.html
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VERSION
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AUTHORS
TITLE
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AI246239 qi29904.x
AI395609 qq42207.x
AI952550 wq42203.x
AI654552 wb48b12.x
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385.170 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB e Maximum DB e

Database

Result 8

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were made in vitro. Following MAP purit faction, this DNA
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consisted of I.M. A.C. & Consess of the process of th
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Email: cgapbe-rémail.nih.gov.
This alone is available royalty-free through LLNL; contact the
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TRAGE Consertium (info@anage llnl) gov) for further information.
Tinsert Length: 921 Scd Error: 0.00
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(note="vector: pryTiD-puc (Pharmacia) with a modified
polylinker; lst etrand clNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I =
oligo(dT) primer: Doubln-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), disperted with Not I and cloned
into the Not I and Eco RI sites of the modified prima
vector Library is normalized Library was constructed by
Bento Scares and M. Patina Bonaldo. "
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Ti Obace; Lo 311)

Ti Obace; Lo 312, Marcia, Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Berdin, S., Costa, F.P., Madai, M.A., Bardin, S., Costa, F.P., Brunstein, S., Singson, D.H., Brunstein, A., deoliveira; F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentan, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Pel: +55-11-2704922
Enail: adiposolation of the FAPESP/LICR Human Cancer Genome Project. This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL Arths entry can be seen in the following URL 400-006-filesize actor can be seen in the following URL 400-006-filesize actor and forward High quality sequence start: 11
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Rua Prof. Antonio Judene 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Trace considered overall poor quality insert Length: 76 Std Error: 0.00 Seq primer: -40m.3 fwd. ET from Amersham High quality sequence scop: 1. Locetion/Qualitiers
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashingron University Genome Sequencing Center
Clone distribution. MCI-CGAP Clone distribution information can be
Clone distribution. MCI-CGAP Clone distribution information can be
Clone distribution. BCI-CGAP Clone Gistorian/LLNL at:

www-bio.lnl.gov/bbrp/finage/image.html
Insert Length: 770 Std Error: 0.00
Seq prime: -40UP from Gistor.

location/Qualifiers
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                                                                                                                                                       Email: cgapbe-remail.nih.gov
Trisne Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emert-Buck, M.D., Ph.D.
GDRA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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Tissee Producement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaido, Ph.D.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 410)
NGI.CGB, bttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clome=IMAGE:2413949"
/clome=IMAGE:2413949"
/clome=IMAGE:2413949"
/clissue_type="pooled germ cell tumors"
/lab.bost=TDH108"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1339609 191 bp mRNA linear EST 29-DEC-1998 (qq22407.x1 Scares NhiMPu B131 and spiens cDNA clone INAGE.1335156 3' similar to 58:MINK HUMAR P13381 15K SLOW VOLTAGE-GATED POTASSIUM CLANNIEL PROTEIN ; mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ad xref="taxon:s606"

Aclone="INAGE:1935156"

Aclone="INAGE:1935156"

Aclone="Inages"Pooled human melanocyte, fetal heart, and

Acceptant urecurs"

Abb. host="DB108"
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similar to SW-HINK HIDMN P1388 ISK SLOW VOLTAGE-GATED POTASSIUM
STANNEL PROFEIN ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Enall: ogspbr remail nin.gov
This clone is available royalty-free through LINL; contact the
IMAG Conscrium (infocanage linl.gov) for further information.
Seq primer: 400P from Gibbo.
                                                                                                                                                                                                                                                                                                                                                                                                         l (bases 1 to 391)
NOI-CGAP bttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Location/Qualifiers
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                      CTCATGGTGATGATTGGAATG 133
   21
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   CTCATGGTGATGATTGGAATG
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AI962650.1 GI:5755363
                                                                                                                                                                                                                                                  AI339609
AI339609.1 GI:4076536
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Unpublished (1997)
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cDNA Library Arrayed by: Greg Lennon, Ph.D.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ઠ a

Gaps

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Length 803

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('intrp://deprs.washington.edu/wentures/collabrrdiscert/hidex.hidex.htm*http://deprs.washington.edu/wentures/collabrrdiscert/hidex.htm*htm;hidex.depusce quality sessessment and vector trimming were conducted unity the mory section of the polynomial programmetes were set to ensure an overal trimmed quality of 97.5 to Debter without any vector fragments in the chosen poly.set or better without any vector fragments in the chosen the polyn-quality region of each sequence. Low-quality best better the high-quality region were replaced with N's to serve
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Tissues Germinated seed and seedlings [1, 2, 8, 11 DAG),
Mixed mature tissures [17, 21, 38, 69, 77 DAG), Kernels
[3, 5, 10, 15, 5, 25, 36, 10, DAP), Adventious roots (6E DAG)
Tasel (3.39 cm, 53 and 56 DAG), Immature ear (0.2.30
cm, 53, 56, 59 DAG), Hask (73 DAG), Sitk, unpollinated
Efficie as an shank etiolated seedlings, callus,
NAR (Asaphthalen seedlings, Anaerobic treated seedlings,
Kinelin-Treated seedlings, ACPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EM266405 478 bp mRNA linear EST 02-JUL-2002 MEST380-D03.T3 ISUM5-RN Zea mays CDNA clone ME80-D03 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryoʻca, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Sprantophyta, Magnoliophyta; Lillopida, Poales; Poaceae; PACC
Glade; Pantooldeae, Andropogonae; Zea.
cell type indicated is HT1080, since a random activation method was used, these sequence taga are not necessarily experested in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iowa State University
G405 Agronov, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-2035
Fax: 515-294-2299
Email: echnalledistatte.edu
Individual besecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 478)

Wen,TJ, Qiu,P, Guo,L, Ashlock,D,A and Schnable,P.S.
Expressed Sequence Tage from BT3 Maize: various stages and
including seedings treated with a variety of hormones
(mpublished (2001)
                                                                                                                                                                                                                                                                                                     0; Indels
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG)
Location/Qualifiers
                                                                                                                                                                                                                              12;
                                                                                                                                                                                                          upery Match 100.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 42; Matches 21; Conservative 0; Mismatches
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/clone="ME80-D03"
/clone_lib="ISUM5-RN"
/tissue_type="mixed"
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/cultivar="B73"
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Schnable Laboratory
                                                                                                                         171 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 CTCATGGTGATGGAATG 511
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                                                                                                                    172 c
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BM266405.1
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/clone="INAGE:Jauberges"
/clone="Inages"@colled_genm cell tumore"
/tissue_type="mooled_genm cell tumore"
/lab host="Mellos"@colled_genm cell tumore"
/lab host="Mellos"@colled_genm cell to proper cell to polylinker; site_1: Note It Site_2: Ec RI; Plasmid DNA from the normalized library NoT_CAP_GG4 was prepared, and sen circles ware made in vitro. Pollowing APP putfication, this DNA was used as tracer in a subtractive hybridization than DNA was used as tracer in a subtractive hybridization reaction. The driver want PCR amplified connas from a pool of 5,000 clones made from the same library (clonelle of 5,000 clones made from the same library (clonelle of 5,000 clones made from the same library (clonelle Subtraction PS) and 104 to their Bonaldo. "

Subtraction PS and 
     MAN Sequencing by: Washington University Genome Sequencing Center Clone distribution NCI-CGAP clone distribution information can be found through the I.M. A.G.E. Comportium/Lubh at: www-bio.llnl.gov/borp/lange/hage/hagen.html
Insert Length. 771 Scd Exror: 0.00
Seq primer: -400P From Gibbo.
High quality sequence stop: 411.
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Harringcon, J. . Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Carl, S., Lewenthal, C., Thorncon, M., Ramachandran, R., Whitrington, J. . Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, F., Valoso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher Creation of genome-wide protein expression libraries using random activation of gene expression
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/ Organisms="Mono capient"
/ Organisms="Mono capient"
/ Colon ilbs="Atherye RAGE Library"
/ Colon ilbs="Atherye RAGE Library"
/ Colon ilns="HT1080"
/ Colos="See "Crastion of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression
/ Nature Biotechnology, in press. Note that even though the
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Mammalia, Eutheria, Primates, Cutarrhini, Hominidae, Homo.
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RST27654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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21227151
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(chitp)//depie weahington edu/sentures/collabir/direct/index.htm.#b but Overall sequence quality sessement and vector trimming were conducted using the Lucy software (chitup://www.tigr.org/sectlab/). 10.75 or using the Lucy software or organization organization of the collaboration parameters were set to ensure an overall trimmed quality of 17.5 or better without any vector fragments in the chosen.
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Spematophyta; Magnollophyta; Lilopeida; Poales; Poaceae; PACC
Slade; Panicoldeae; Andropogoneae; Zea.
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seadlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
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Lowa State University, Ames, IA 50011-1010, USA
Tel: 512-54-0975
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                                                                                                                                                                                                                                                                                                                                                                                                                      87.6%; Score 18.4; DB 13; Length 478; 95.0%; Pred. No. 4.9e+02; tive 0; Mismatches 1; Indels 0
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BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
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117 c 133 g 127 t
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/cultivar="B73"
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Contact: Patrick S. Schnable
Schnable Laboratory
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force-vector: pr7719AC; Site_1: BcoRI; Site_2: NotI;
fistures: Germinate seed and seedlings (1, 2, 8, 11 DAG),
Kissures: Germinate seedlings (1, 2, 8, 11 DAG),
Kissures: Germinate (1, 21, 31, 69, 77 DAG), Kornels
(3, 5, 10, 11, 20, 23, 30, DAB), Adventious roces (65 DAG),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0, 2-6),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0, 2-6),
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Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0, 2-6),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0, 2-6),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0, 2-6),
Tassel ear shank, early Andersonic reacted seedlings,
Nimelin-trasted seedlings, And (abmature) early early trasted seedlings,
Tassel early and (sabmarel) of (sibberellic acid) -trasted
Seedlings, AN (abmature as follows: First-strand CDNA molecules were generated as follows: First-strand CDNA was prepared for prine of the prine of the constant of the con
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Fax: 650 725 8221
Fax: 650 725 8221
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Plate: 683008 row: B column: 08.
Location/Qualifiers
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Contact: Walbo
Department of Biological Sciences
Stanford University
/clone lib="ISUM5-RN"
/tissue_type="mixed"
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/cultivar="B73"

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/ABD_NOSE="Unique" in the property of the prop
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Permatophyta, Magnoliophyta; Liliopsida, Poales; Poaceae; PACC
clade; Panicoideae, Andropogonae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases it c.955)
Wen. T., Qiu.F., Guo.L., Ashlock.D.A and Schnable.P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0978
Pax: 515-294-2299
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PORTABLE primer T7-1 (AA TAC GAC TCA CTA TAG)
PORTABLE primer T3 (ATT AAC CCT CAC TAA AG)
Seg primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/clone="MEST275-A06"
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/tissue_type="mixed"
/lab_host="DH10B"
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/cultivar="B73"
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Schnable Laboratory
                                                                                                                                                                                                                                                                                                                               GI:18176183
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AUTHORS
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/db xref="taxon:4577" /clone_lib="683 - 14 day immature embryo from Hake lab (HS
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/clone_lib="683 - 14 day immature embryo from Hake lab (HS
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                                                                                                                                                                                                                                                                             //oce="Cream embryo, Wictor: pBKCMW (Stratagene's Zap
Bkpress); Site_1: XNo1; Site_2: EGORI; Directionally
cloned, 14 day immature embryo library created with
Stratagene's Zap Expensi CDNA protocol."
I 13 1 146 9 143 t lothers
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//dew_stage="+daya_ster_pollination"
//dew_stage="+daya_ster_po
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Malze ESTs from various cDNA libraries sequenced at Stanford
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Pred. No. 5.3e+02;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.6%; Score 18.4; DB 10; Length 542; 95.0%; Pred. No. 5.2e+02;
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/lab_host="DH10B"
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Plate: 683028 row: H columr
Location/Qualifiers
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Fengles Song H., Heang, O., Heang, C. Cu.Y., Yang, Y., Gao, G., Xiao, H., Xi.X., Zi.N., Olan, B., Ling., Qu.U., Go, Y., Cheng, Z., Xu.Z., H., Xi.X., Cheng, Z., Xu.Z., Zhong, M., Zhong, Z., Xu.Z., Zhong, Z., Zhong, Z., Xu.Z., Zhong, Z., Zhong, Zh
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rt). Overall sequence quality assessment and vector trimming were
conducted using the lucy software (<http://www.tigr.org/softlab/>).
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WATTON Gluy, P., Guo, L., Ashlock, D. A and Schnable, P. S.

Wattressed Sequence Tags from B77 Maize: various stages and tissues

Unpublished (2001)
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                                                                                                                 Ekkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases I to 623)
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Schnable aboracory
Towa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel. Si5-294-2299
Fax: 515-294-2299
Enail: schnable@istate.edu
Individual basecall and confidence value were assigned using the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADBDAAA11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 g
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Matches 19; Conserv
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BM351807/c
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then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
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Spermatophyta, Megnoliophyta; Liliopaida; Poales; Poaceae; PACC
Clade; Pailcoideas; Andropogoneae; Zea.
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A77702181 ADB Homo sapiens cDNA clone ADBDAAll 5', mRNA sequence.
A77702181
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//db_xref="texon:14577"
//done lib="683 - 14 day immature embryo from Hake lab
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Walbot,V.
Walse ESTs from various oDNA libraries sequenced at Stanford
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                                                                                                                                                                                                                     Score 18.4; DB 13;
Pred. No. 5.4e+02;
0; Mismatches 1;
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95.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Zea mays"
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Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                 153 c
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AUTHORS
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//issue_type="mixed"
//ab_host="mixed"
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//asues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
//asues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
//asues: Germinated (1, 21, 38, 69, 77 DAG),
//asues: Germinated (2, 5, 30, DAB), Alventious roots (65 DAG),
//asseel (-3, 30 cm, 53 und 56 DAG), Immature ear (0, 2-3.0
//asseel (-3, 30 cm, 53 und 56 DAG), Immature ear (0, 2-3.0
//asseel (-3, 30 cm, 53 und 56 DAG), Immature ear (0, 2-3.0
//asseel (-3, 30 cm, 53 und 56 DAG), Immature ear (0, 2-3.0
//asseel (-3, 40 cm, 53 und 56 DAG), Immature ear (0, 2-3.0
//asseel (-3, 40 cm, 53 cm, 54 cm,
Lucy parameters were set to ensure an overall trimmed quality of 5.74 or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality hases between the poly-T and the high-quality region were replaced with N's to serve
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POLY.
POR BACCETE.
POR PRIMERE
PORMARD: PITIMET 17-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer 13 (ATT AAC CCT CAC TAA AG)
Seg primer: primer 13 (ATT AAC CCT CAC TAA AG)
Location/Qualifiers
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    634
    /organism="Zea mays"
    /cultivar="B73"

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Ouery Match 87.6%; Score 18.4; DB 13; Length 634; Best Local Similarity 95.0%; Pred. No. 5.58+02. Metches 19; Conservative 0; Mismatchios 1; Indels 0;

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0; Gaps

104 TCATGGTGATGATAGGAATG 85

Search completed: June 9, 2003, 10:05:54 Job time : 888 secs

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Sequence 30, App Sequence 32, App Sequence 24, App Sequence 24, App	Sequence 26, Appl Sequence 36, Appl Sequence 56, Appl	Sequence 36, Appl Sequence 56, Appl	Sequence 56, Appl		Sequence 9, Appl1 Sequence 2439, Ap			Sequence 1, Appli Sequence 1. Appli		Sequence 24, Appl Sequence 1. Appli		Sequence 3, Appli	Sequence 3, Appli		13	19	13	4,	Sequence 1, Appli	in i	-i -i	ų,	10,	⋖.	87, A	Sequence 206, App Sequence 9, Appli	210,	Sequence 48, Appl Sequence 22, Appl	22, 4	Sequence 140, App Sequence 7, Appli	15	equence 6,	Sequence 24, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	12	Sequence 13, Appl	-, -,	Sequence 1, Appli	3 3	equence 13
105-005-015-30 Sequence 30, App 105-005-015-32 Sequence 24, App 105-08-147-221B-26 Sequence 24, App 105-08-147-221B-26 Sequence 24, App 105-05-005-051-24 Sequence 24, App	-09-005-051-26 Sequence -09-232-200-36 Sequence -09-232-200-56 Sequence	-09-232-197-36 Sequence -09-232-197-56 Sequence -09-232-201-36 Sequence	-09-232-201-56 Sequence	-09-058-260-1 Sequence	-08-781-802-9 Sequence -09-134-001C-2439 Sequence	-08-793-044-1 Sequence	.08-217-529-1 Sequence	-08-781-802-1 Sequence -08-694-078-1 Sequence	-09-837-863-23 Sequence	-09-837-863-24 Sequence -08-484-105-1 Sequence	-08-484-106-1 Sequence	-08-092-817-3 Sequence	-09-091-432-3 Sequence	-08-596-366-1 Sequence	-08-714-918-19 Sequence 19	Seguence 19	-09-266-417-19 Sequence 19	-08-404-445-1 Sequence 1, -08-233-008A-7 Sequence 7,	٦, ٥	-08-250-848-2 Sequence 2,	Sequence 1, Sequence 1,	Sequence 1,	Sequence 10,	Sequence 3, A	Sequence 87, A	Sequence 206, Sequence 9, Ap	Sequence 210,	Sequence 48, Sequence 22,	Sequence 22, A	Sequence 140, Sequence 7, Ap	Sequence 15	Sequence 6,	Sequence 24	Sequence	Sequence	Sequence 1	Sequence 13	Sequence 13	Sequence 1,	Sequence 1,	Sequence 18	Sequence 13
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Sequence 11, Appl Sequence 55, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 59, Appl Park (No. 51945) Sequence 10, Appl Sequence 10,	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	sequence 30, Appl sequence 31, Appl Sequence 51,	Sequence 9, Appliagement of Appliagement 12, Appliagement 12, Appliagement No. 526635 Sequence 13, Appliagement 1, Appliagemen	400000044444441116000446
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Sequence 71, App Sequence 55, App Sequence 2, Appl	Sequence 15, Appl Sequence 28, Appl	28,	Sequence 28, Appl Sequence 2, Appli	٠ <u>,</u>	Sequence 5, Appli	ີ່ທີ		Sequence 5, Appli	Sequence 127, App	Segmence 5. Appli	Sequence 5, Appli	Sequence 19, App.	Sequence 19, App	Sequence 81, Appl	Sequence 7, Appri	Sequence 13, Appl	Semience 5, Appli	Semience 174. Ann	Sequence 174, App	Sequence 6, Appli	Sequence 21, Appl	Sequence 21, Appl	Sequence 24, Appl	Sequence 24, Appl	Segmence 3 Appli	Sequence 3. Appli	N.	m	ď,	ά,	Sequence 13, Appl		19,	83, A	Sequence 26, Appl	ຸຕ	4.	4.	⊣ თ			23,	Sequence 23, Appl	52, 4	51, 7	'n.	'n.	in	Sequence 5, Appli	ີພ	N.	Sequence 22, Appl	₹.	Sequence 1, Appli	, r	'n,	7,
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Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli	20,	9,	Sequence 46, Appl	46,	Sequence 46, Appl	334	42,	'n.	Sequence 4, Appli	, 4	4	H)	22	Sequence 22, Appl	ì ~	9.6	9.4	34	67,	20,	304,	m ·	٦,	Seguence 1, Appli	4 C	46	74	Sequence 77, Appl	74,	50	63	Sequence 2, Appli	'n	Sequence 7, Appli	Sequence /, Appli	Ä	Sequence 4, Appli	Sequence I, Appli	Sequence 10. Appl	10,	4,	4	Sequence 4, Appli	'n	۲,	Sequence 1, Appli	equence 1,	Sequence 1. Appli	ì'n	6	'n	r ,	Sequence /, Appli		1, 1	e 1,	Sequence 1, Appli
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APPLICANT: THOSTERE FOX. AULT
APPLICANT: THOSTERE FOX. AULT
APPLICANT: Lepine, OLylaine
APPLICANT: Lepine, OLylaine
APPLICANT: Hain Nainting
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APPLICANT: Hain SINGRED FOX THOSE
APPLICANT: Partit, Oosebh
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: A PROBES 12
CORRESPONDENCE APPLICANT HAIL OF STEECT. SERVICE AND THE STEECT SERVICE AND THE SERVICE AND T
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels
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COUNTRY: USA

CONTRY: USA

CONTRY READALE FORM:

CONTRY READALE FORM:

CONTRY READALE FORM:

APPLICATION NUMBER: USA

FILING DATE: USA

FI
REFERENCE/DOCKET NUMBER: UF15.C3
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Sequence 5, Application US/08353485

Patent No. 5830710

GENERAL INPORMATION

APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1627 GCTGGAAGACGTCTTCCG 1610
                          TELECOMOUNICATION INFORMATION:
TELEPRONE 1994 375-8100
TELEPRON 1994 375-800
INFORMATION FOR SED, DAG: 5:
SEQUENCE CHARACTERISTICS:
LEWGTH 1641 base pairs
TYPE: HIGHEL acid
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TELEPAX. (904) 372-8800
INFORMATION FOR ESQ ID NO: 5:
SEQUENCE CHARACTERSTICS:
LENGTH: 1841 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 18; Conservative
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LOCATION: 374..1424
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MEDIUM TYPE: PLOMPY disk
COMPUTER: PLOMPY disk
COMPUTER: PROSPINE PROSPINE DOSSING-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.25
CURRAT APPLICATION DATA:
APPLICATION MUMBER: US/08/570,331
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US-09-109-5.0.4
US-09-109-9.7.4
US-09-109-9.7.4
US-08-29-6.0.7
US-08-29-6.7
US-08-20-7.7-13
US-09-07-13
US-09-07-13
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US-09-07-13
US-09-07-13
US-09-07-13
US-09-08-78-13
US-09-07-13
US-08-26-18
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US-09-526-993-5
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US-08-532-795-24
US-07-971-160-9
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US-08-465-273-9
US-09-119-024-9
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CLEASTRICATION: 42
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 42
PRIOR APPLICATION HORBER: US 08/353,485
CLASSIFICATION HORBER: US 07/647,119
FILING DATE: 25-JAN 1991
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION DATA:
TILING DATE: 09-SEP-198
ATTORNEY/ARBER: US 07/241,640
ATTORNEY/ARBER: US 07/241,640
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REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
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APPLICANT: Defer, Thomas L. THILLOS TWONTHING ENZYMES THILLOS TWANTHOOD OF PRODUCING AND PURIFYING ENZYMES CORRESPONDER DAPERS: 4 CORRESPONDER DAPERSS: 4 CORRESPONDER DAPERSS:
                                                            GENERAL INFORMATION:
APPLICANT: Deite, Thomas L.
TITLE OF INVERTION: METHOD OF PRODUCING AND PURIFYING ENZYMES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4%; Score 17; DB 1; Length 249; 100.0%; Pred. No. 5.6; ive 0; Mismatches 0; Indels
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CITY: Milwaukee
COUNTRY: Misconain
COUNTRY: U.S.A.
ZIP: 5302-4497
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
MEDIUM TYRE: Ploppy disk
OCHUPUTER: IMP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC-Compatible
COMPATING SISTEM: PC-COS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 660336.90489
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUSTRANT. TEACHILIN REGERGE #1.0, N. CUSTRET APPLICATION NUMBER: PCT/US96/00728 FILING DATE: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: NAME: BAKET, Jean C.
                                                                                                                                                                  E: Quarles & Brady
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Quarles & Brady
411 East Wisconsin Avenue
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; GENERAL INFORMATION:
  US-08-378-698-2/c; Sequence 2, Application US/08378698; Patent No. 5766914
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
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; MOLECULE TYPE: DNA (genomic)
US-08-378-698-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles &
                                                                                                                                                                                                              CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                      RY: U.S.A.
53202-4497
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                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3. Application US/08446794A
Patent No. 2547327
GENERAL INFORMATION:
APPLICANT: UEXT, UNIVERSEL SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCE SEQUENCES 1
TITLE OF INVENTION: PROSPHOLIPASE D GENE ORIGINATED FROM TITLE OF INVENTION: PROSPHORES;
CORRESPONDENCE ADDRESS;
ADDRESSEE: P.O. BOX. 47
CITT: FALLS GHURCH, STEMART, KOLASCH AND BIRCH
                                                                                                                                                                  Score 18; DB 2; Length 1841; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.9%; Score 18; DB 1; Length 2804; 100.0%; Pred. No. 1.7;
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                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747
COMPUTER READARDE PORM: :
MEDIUM TYPE: Ploppy disk
COMPUTER: IM PC COMPALIALIE
COMPUTER: IM PC COMPALIALIE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. w.
                                                                                                                                                               Query Match 9.9%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 1.7 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPICATION: 536
ATTORNET AGENT INFORMATION:
NAME: MUREHY JR. GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0760-0203P
TELECPHONNICATION INFORMATION:
TELECPHONE: 703-205-8050
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             1627 GCTGGAAGACGTCTTCCG 1610
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                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 18; Conservative
STRANDEDNESS: single
                                                                                 CDS
374..1424
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                             US-08-446-794A-3/C
                                                                              ; NAME/KEY:
; LOCATION:
US-08-353-485-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-446-794A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Burges, Christopher C.
APPLICANT: Garion, Theodore J.
APPLICANT: Carion, Theodore J.
APPLICANT: Devil, Adnan
APPLICANT: Peril, Adnan
APPLICANT: Nord, Donna M.
APPLICANT: Nord, Donna M.
APPLICANT: Schiegel, Robert
TITLE OF INVENTION NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: ROOUCTS
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B.8%; Grore 16; DB 4; Length 622;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels

Matches 16; Conservative 0; Mismatches 0; Indels
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APPLICANT: CAHOON, Rebecca E.
APPLICANT: CAHOON, Rebecca E.
APPLICANT: CAHOON, Rebecca E.
APPLICANT: Refalls, AHTONI
TITLE OF INVENTION: Transcription Coactivators
TILLS OF INVENTION: Transcription Coactivators
CURRENT APPLICATION NUMBER: USy00/342,648
CURRENT APPLICATION NUMBER: 1990-6-29
EARLIER PILING DATE: 1990-6-29
EARLIER PLING DATE: 1009-6-29
SOFTWARE: Microsoft Office 97
LENGARE: Microsoft Office 97
LENGARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REPERVE: CCD-257 (18)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER PELLON NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FetESD for Windows Version 3:0
                                                                                                                                                                           ; Sequence 381, Application US/09328111; Patent No. 6262333; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(622)

COTHER INFORMATION: n = A,T,C or G
US-09-328-111-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09342648
Patent No. 6248584
                                                    2290 GCTGGAAGACGTCTTCC 2306
      24 GCTGGAAGACGTCTTCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 TTATATGGACAATTGG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 TIATATGGACAATTGG 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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NAME/KEY: unsure
LOCATION: (1621)
                                                                                                                                                         US-09-328-111-381/c
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US-09-342-648-7/c
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LENGTH: 622
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                                                                                                                                                                                                                                                                                                                                                         Omery Match 9.4%; Score 17; DB 5; Length 249; Best Local Similarity 100.0%; Pred. No. 5.6; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: USKY, JUN
APPLICANT: USKY, JUN
TITLE OF INVENTION, PHOSPHOLIPASE D GENE ORIGINATED FROM
TITLE OF INVENTION: PLANT
WINNER OF SEQUENCES: 7
CORRESPONDENCE S. 7
ADDRESSEE, BIRCH, STEWART, KOLASCH AND BIRCH
STERET: P. 0. BOX 747
CITYS: FALLS CHURCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP. 22940-0797
COMPUTER READALE FORM:
MEDIUM TIPE: FLORDY disk
COMPUTER: 18MP FOC COMPACTIBLE
COMPATING SYSTEM: FC-DOS/MS.DOS
SOFWMASE: ParentILI Release #1.0, Version #1.30
SOFWMASE: ParentILI Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/446,794A
FILING DATE:
REGISTRATION NUMBER: 35,433
REPERANCE/DOCKET NUMBER: 66036.90489
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECHAN: (414) 277-5709
TELECHAN: (414) 217-5509
TELERAX: (414) 217-552
INFORMATION FOR EQI IN NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 base pairs
TYRE: NUCLEIC acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MORENT TA, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/JOCKET NUMBER: 0560-0203P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08446794A Patent No. 5747327 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATGGACAATTGGCGCCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 Arggacaarrggcgcca 47
                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA (genomic)
PCT-US96-00728-2
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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SEQUENCE CHARACTERISTICS:
LENGTH: 2804 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703-205-8050
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STRANDEDNESS: single
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107..2542
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                                                                                                                                                                                                                                                              ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-446-794A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICAMY: C. Frank Bennett
APPLICAMY: Elizabeth J. Aktermann
APPLICAMY: Elizabeth J. Aktermann
APPLICAMY: Elizabeth J. Savya
APPLICAMY: List C. Savya
TITLE G. WINGHTON ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REFRENCE: 15F4-048
FILE REFRENCE: 15F4-049
FILE REFRENCE: 15F4-049
FILE REFRENCE: 15F4-049
FILE REFRENCE: 10F4-049
FILE REFR
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100.0%; Pred. No. 20;
tive 0; Mismatches 0; Indels (
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; Sequence 994, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/09496694B; Patent No. 6335194; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10809 ATTTTTATTACTTATA 10824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10809 ATTITIATTACTIATA 10824
        2000-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 ATTTTTATTACTTATA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (11955)...(12044)
US-09-630-706-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (11955)...(12044)
US-09-496-694B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 16; Conservative
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: CDS
: (3174) ... (3283)
: CDS
: (5158) ... (5275)
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                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (2811)...(2921)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                      (3174)...(3283)
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (5158)...(5275)
NAME/KEY: CDS
                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
    CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 10
                                                                                                   LENGTH: 14796
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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US-09-630-706
US-09-630-706
US-09-630-706
US-09-630-706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROFISIN THAT INHIBITS
TITLE OF INVENTION: CELULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 16; DB 4; Length 14796;
100.0%; Pred. No. 20;
iive 0; Mismatches 0; Indels
                                                            Query March

8.8%; Score 16; DB 4; Length 1626;
Best Local Similarity 100.0%; Pred. No. 20;
Best Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE Reteard Relaying Relaying Software Relaying Relaying Marker Application Number: 0808/975,080 RIBERT APPLICATION NUMBER: 0808/975,080 RIBERT RELAYING NUMBER: 0808/1975,080 RIBERT RELAYING NUMBER: 080/031,435 RAPLICATION NUMBER: 080/031,435 RAPROMENTAGENT NUMBER: 080/031,435 RESERVED FORCER NUMBER: 044874-5022-01-WO TELECOMONICATION NUMBER: 044874-5022-01-WO TELECOMONICATION NUMBER: 044874-5022-01-WO TELECOMONICATION NUMBER: 0427-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/08975080 Patent No. 6245523 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10809 Artritarractiana 10824
                                                                                                                                                                                                                       1166 ACAGCTGAGCAAGAGG 1151
                                                                                                                                                                                         85 ACAGCTGAGCAAGAGG 100
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 ATTTTTATTACTTATA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 14796 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Conservative
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ADDRESSEE: MORGAN, LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                              US-08-975-080-35
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US-09-342-648-7
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Sequence 114, Application US/08961527
Sequence 114, Application US/08961527
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1854;
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
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                       CURRENT APPLICATION NUMBER: US/09/134,001C
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STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15;
Pred. No.
                                                           CURRENT FILING DATE: 1999-00-13
PRIOR PELLANG DATE: 1999-10-10
PRIOR FILING DATE: 1999-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-06-14
NUMBER OF SEQ ID NOS: 5674
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; P. Matches 15; Conservative 0;
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TELEFAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36,373
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1750 GTACCTCATGGTGAT 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 GTACCTCATGGTGAT 161
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2069 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION NUMBER:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-961-527-174/c
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APPLICANT: ROBE, BINCE C.
TITLE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDINCE ADDRESS:
ADDRESSES: MORRISON & POERSTER STREET: 755 PAGE MILL ROAD
CITY: PAGE ALLO ROLL ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEG for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIGRAPHICATION INTA:
PRIGRAPHICATION INDEES:
FILING DARE:
PRIGRAPHICATION NUMBER:
PRIGRAPHICANION NUMBER:
PRIGRAPHICATION NUMBER:
PRIGRAPHICANION NUMBER:
PRIGRAPHICATION NUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPAN: 06141
INPORMATION FOR SERIESTICS: SEQUENCE CHARACTRISTICS: LIGARATTRISTICS: TYPR: nucleic stid stransmission double stransmission double monitoff; itenimical included the monitoff inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 CCCTCCAAGCCAAAG 115
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                                                                                                                                                                                                                                                                                                                          STATE: CA
COUNTRY: USA
ZIP: 94304-1016
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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LOCATION: 1...797
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ANTI-SENSE: UNKNOWN
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CLASSIFICATION:
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Gaps

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Indels

8.3%; Score 15; DB 4; Length 2069; 100.0%; Pred. No. 67;

100.0%; Pred. No. 67; tive 0; Mismatches

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GERREAL, INFORMATION:
APPLICANT: LyAN DOUGELE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC-007

Sequence 1175, Application US/09134001C Patent No. 6380370

US-09-134-001C-1175

RESULT 13

15; Conservative

Best Local Similarity

Query Match Matches

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LENGTH: 3258 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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67;
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US-08-804-439A-12/c
Sequence 12, Application US/08804439A
Sequence 13, Application US/08804439A
Sequence 13, Application US/08804439A
Sequence 13, Application US/08804439A
APPLICANT: Bose, Timochy W. APPLICANT: Bose, Marrix L. APPLICANT: Secol, Marrix L. APPLICANT: Secol, Marrix C. ITTLE OF INVENTION: GINCORPOTEIN B OF THE RFHV/KSHV
ITTLE OF INVENTION: SUBFAMILY OF HERPES VIRUSES
NOMBER OF SEQUENCES: 113
ADDRESSEDNENCES: 113
ADDRESSEDNENCES: ADDRESSED EXCENTIVE SQUARE, SEC 1400
CITY: La Oblia
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDION TYPE: FLORDPy disk
MEDION TYPE: FLORDPy disk
COMPUTER. IMB PC COMPALIDLE
COMPUTER: THE PC MEDION TO THE
SOFTWARE: PLEGETIN RELEASE #1.0, Version #1.30
CHRENY ADDICATION NUMBER: US/08/604,439A
CLASSIFICATION WINGER: US/08/604,439A
CLASSIFICATION HOPPAMITON:
NAME: Halle, Lisa A.
RAFELSENCY/DON/UNERR: 09176/00401
TELECOMMUNICATION INPORMATION:
TELESPA: (679-507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08720229
Patent No. 602542
GENERAL INFORMATION:
APPLICANT: Rose, Timothy M.
APPLICANT: Bosch, Marnix L.
APPLICANT: Strand, Marnix L.
APPLICANT: Strand, Kurt
APPLICANT: Strand, Kurt
APPLICANT: Strand, Kurt
APPLICANT: STRAND, SURFANIION: SURFANING OF THE RFHV/KSHV
TITLE OF INVENTION: SUBFANIIX OF HERDES VIRUSES
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.3%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 67; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 ATTGGAATGTTCTCT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison
STREET: 755 Page Mil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-804-439A-12
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ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-720-229-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                               92037
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GENERAL INCOMMITON:
APPLICANT: Birnbamer, Lutz
APPLICANT: Birnbamer, Lutz
APPLICANT: Birnbamer, Lutz
APPLICANT: Birnbamer, Lutz
APPLICANT: Will Xi
TITLE OF INVENTION: Capacitative Calcium Ion Enry Into Mammalian Cells
TITLE OF INVENTION: Essential for Agonist-Activated Capacitative Ca2,
NUMBER OF SEGUENCES: 32
CORRESENDENCE ADDRESSS:
ADDRESSEE: Pons, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/720,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 3;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGRET INFORMATION:
NAME. SCHIEF, J. MICHAEJ
REGISTRATTON NUMBER. 40, 253
REFERENCE/DOCKET NUMBER. 29938-20002.00
TELECOMMUNICATION INFORMATION:
TELEBRAY 811-560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP. 1906— COMPUTER READABLE PORM: MEDIUM TREADER PROPOSITION OF COMPUTER COMPUTER COMPATION OF COMPUTER COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIPIONTION 1435
PRICHARION DATA APPLICATION DATA APPLICATION DATA SOLVED APPLICATION TOWNER: 60/025,111
RIGHTON TOWNER: ANGRES APPLICATION NAME: OTHER APPLICATION NAME: OTHER APPLICATION NAME: OTHER APPLICATION NAMES
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 2, Application US/08729955A
; Patent No. 5932417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 120:
TELECOMMUICATION INFORMATION
TELEBHONE: (110) 788-5000
TELEBHONE: (110) 77-1297
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2608 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 ATTIGGAATGTTCTCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 ATTGGAATGTTCTCT 754
                                                                                                                                                                            26-SEP-1996
V: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: USA
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                            FILING DATE: 26
CLASSIFICATION:
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US-08-720-229-12
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GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTOR: Streptococcus pneumoniae Polynucleotides and Sequences
TITLE OF INVENTOR: Streptococcus pneumoniae Polynucleotides and Sequences
TITLE OF SEQUENCES: 331
CORRESCONDENCE ADDRESS:
STREET: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: ROCKVILLE
STREET: Waryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137, Application US/08961527
Parent No. 6420135
GBNERAL INFORMATION
THORMATION: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 191
CONRESPONDENCE ADDRESS: 100
ADDRESSES: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 4965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP VECTA 486/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 68;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                      MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                   ; Sequence 143, Application US/08961527; Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTONEY (AGENT INFORMATION:
NAME: BTOOKES, A. ANGES
REGISTRATION NUMBER: 36.373
REPERRACE/DOCKET NUMBER: PB34
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.3%; Scc
Best Local Similarity 100.0%; Pi
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4533 TGATTGGAATGTTCT 4519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 TGATTGGAATGTTCT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .: 4965 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-961-527-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
US-08-961-527-143/c
                                                                                                                                                                                                                                                          20850
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                                                                                                                                                                                                 DB 2; Length 3258;
68;
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100.0%; Pred. No. 68;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Wei-Len
APPLICANT: Olinan, Alfred G.
TITLE OF INVENTION: SOUGHEE WAWALIAN ADENVLYL CYCLASE
TITLE OF INVENTION: NOW USBS THEREFOR
NUMBER OF SEQUENCES: 11
ADDRESSED: ATTOID, White & Durkee
STREET: RO. Box 4433
CITY: Housen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642 REFERENCE/DOCKET NUMBER: UTS0:450 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Texas
COUNTRY: United States of America
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             2232 ATGATTGGAATGTTC 2246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 CTCCAAGCCAAAGTT 117
                                                                                                                                                                                                                                                                               160 ATGATTGGAATGTTC 174
                                                                                                                                       ; INDIVIDUAL ISOLATE: Mtrp4
US-08-729-955A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.33
Best Local Similarity 100.4
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-726-214-7
                     TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                           2
                                                         HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-726-214-7
                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
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FILING DATE:

◆ RESULT 19

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Gaps
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hartis Ph.D., Stephen E.
APPLICANT: Mandy W.D. Gregory R.
APPLICANT: Good-Choudhury Ph.D., Mandini
APPLICANT: FOR Ph.D. Usin On., Mandini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
TITLE OF INVENTION: GIRCGENIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%; Score 15; DB 3; Length 15144;
100.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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PAREAT NO. 2553560
GENERAL INFORMATION
APPLICANT Chamber-fail, Jeffrey S.
APPLICANT Henser, Michael A.
APPLICANT HENSER A.
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/458,434A
APPLICATION NUMBER: US/08/458,434A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P00060US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: James C. Weseman, Esq. 401 B. Street, Suite 1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

CLASSIF FORTION: 415
ATTORNEY AGENT INFORMATION:
NAME: Wescenant, James C.
REGISTRATION NUMBER: 90.507
REFERENCE/DOCKET NUMBER: 90.007
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 61-56-1048
INFORMATION FOR EGO ID NO: 6: SEGUENCE CHARACTERISTICS:
LENGTH: 15144 Dase pairs
TYPE: NUCLEIC CANIB.
                                                                                                                                                                                                                      US-08-458-434A-6/c
; Sequence 6, Application US/08458434A
; Patent No. 6083690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4226 GACGTCTTCCGAAGG 4212
                                                                 8919 ACTITATCCAATITC 8905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GACGICITCCGAAGG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: James C. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C
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US-08-735-609-4
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Estern No. 420135
GENERAL INFORMATION
FALL SECONDAL TO Charles Winsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
CORRESPONDENCE ADDRESS;
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Pred. No. 69;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 69;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                               PB340P1
                                                                                                                                                NAME: Brookes, A. Anders
NAME: Brookes, A. Anders
REGISTATION NUMBER: 5, 5333
REFERENCE/DOCKET NUMBER: 9, 5334
RELECOMMICATION INFORMATION:
TELECOMMICATION INFORMATION:
TELECHONE: (301) 309-8512
INPORMATION FOR SEG 1D NO: 137;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512
INFORMATION FOR SEQ 1D NO: 128:
SEQUENCE CHARACTERISTICS:
LENGTH: 13440 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10747 GGTGATGATTGGAAT 10761
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 GGTGATGATTGGAAT 170
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12666 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.3%
Best Local Similarity 100.(
Matches 15, Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-961-527-137
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WEDING TYPED, FLOODY diek
CMRUTTER: TBM PC compatible
OPERATING SYETER: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Chamberlain, Jaffrey S.
APPLICANT: Mallitano, Addrea
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
THILE OF INVENTION: INPROVED ADENOVIROS VECTORS
                                                                                                                                                                                                                                                                  DB 2;
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3%; Score 15; DB 3;
100.0%; Pred. No. 70;
tive 0; Mismatches
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ADDRESSES:
STREET: ARGIAN & CARTOLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                        Score 15;
Pred. No.
                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
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     (415) 705-8410
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DESCRIPTION: /desc = "DNA"
                                    INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
                                                                                                                                                                                                                                                 8.3%; SCOL.
100.0%; Pre
0;
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Patent No. 6057158
GENERAL INFORMATION:
                      397-8338
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REGISTRATION NUMBER: 40,027
                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UNTELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.(
Watches 15, Conservative
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APPLICATION NUMBER: US.
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Best Local Similarity 100.
Matches 15, Conservative
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EDNESS: double
                         (415)
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     TELEPHONE:
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                      ELEPAX:
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CLASSIFICATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Kumar-Singh, Rajendra
Annar-Singh, Rajendra
TITLE OF HWENTON: IMPROVED ADENOVIRUS VECTORS
CORRESPONDENCE SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, Li.P
STREET: 220 Montgomery Street, Suite 2200
                                                                                               COMPUTER FRAMELE FORM:
MINITOR TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-1005/MS-1005
SOFTWARE: Patentin Release #1.0, Veruion #1.30
CURRENT APPLICATION DATA:
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: 220 Montgomery Street, Suite 2200
San Francisco
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8.3%; Score 15; DB
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches
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FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States Of America
                                                                                                                                                                                                                                         FILING DATE:
CLASSIFECATION: 455
CLASSIFECATION: 455
ATTORNEY/AGENT INFORMATION:
NAME: INFORMATION:
REDEFENCE/DOCEAT NUMBER: 40, 027
FELEPHONE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chamberlain, Jeffrey S.
                                                             United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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                                          California
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MOLECULE TYPE:
                                                                              94104
                                                             COUNTRY:
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B.3%; Score 15; DB 3; Length 34303;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 0; Indels 0
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COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQUENCE 4, Application US/09562919
; Patent No. 6415206
; Patent No. 6415206
; Patent No. 6415206
; Patent Chamberlain, Jeffrey S.
; APPLICANT: Chamberlain, Jeffrey S.
; Malitano, Andrea
; Hauser, Witchael A.
; Kumar Singh, Rajendra
Hartigan-O'Comnor, Dennis J.
; TITLE OP INVENTION: IMPROVED ADEMOVIRUS VECTORS
; CORRESPONDENCE ADDRESS;
; ADDRESSEE: Median & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,497
IMPROVED ADENOVIRUS VECTORS
                                                          E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States Of America
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APPLICATION NUMBER: US/09/562,919
                                                                                                                                                                                                                                                                                                                                                                     CLASSITICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: 89 FILING DATE:
ATTORNEY/AGRY INFORMATION:
NAME: INFOILA 18 18 18 E
REGISTRATION NUMBER: 40,02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     United States Of America
                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8439 GACGCTGGAAGACGT 8453
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COMPUTER READABLE FORM:
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                     NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                       San Francisco
California
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                  COUNTRY: UN
                                                                ADDRESSEE:
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US-09-562-919-4
                                                                                                       CITY: S
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8.3%; Score 15; DB 3; Length 34303;
Best Local Similarity 100.0%; Pred. Mo. 70;
Matches 15; Conservative 0; Mismatches 0; Indels (
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WEDLIN TYEE: RIOUPDY disk
WEDLIN TYEE: RIM PC COMPACTION
OFFICIATION SYSTEM: PC-DOS/MS_DOS
SOFTWARE: PACHICIN RELABOR
CURRENT APPLICATION DATA:
PPLICATION NOMBER: US/09/244,752
                                                                                                                                                                                                                                 APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Mathatitano, Addrea
APPLICANT: Hauser, Michael A.
APPLICANT: Warer-Singh, Asjendra
APPLICANT: Warer-Singh, Asjendra
APPLICANT: Hartian-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBERS OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                               E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chamberlain, Jeffrey S.
Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: TIGGILA, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMUNICATION INFORMATION:
TELEFACK: (415) 397-8338
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09245497
Patent No. 6083750
GENERAL INFORMATION:
                                                                                                                                                                       Sequence 4, Application US/09244752
Patent No. 6063622
                                                   8439 GACGCTGGAAGACGT 8453
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                  21 GACGCTGGAAGACGT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 34303 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 220 Montgome
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Chambe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94104
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APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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; Sequence 3, Application US/09563869A
                           Best Local Similarity
Matches 15; Conserva
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US-09-563-869A-3
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                                                                                                                                                                                                                                                                                                                                                                                                         US-08-973-334-3
Query Match
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ZIP: Z2201-4714
COMPUTE READABLE PORM:
COMPUTER: ISOPOPY disk
COMPUTER: ISOPOPY disk
COMPUTER: TOWN PC COMPALBLE
COMPUTER: PC-DOGS/MS-DOS
SOFFWARE: Premit Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/374.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08174481
Parennivo, SABDICATION
PARTICANT GEORGE, SANUEL E.
APPLICANT BLAZING, MICHAEL A.
ITLE OF INVESTION ADSNOVIBAL VECTOR BYSTEM
COMMERCE OF SEQUENCES: 9
CORRESPONDERE ADDRESSES: NIXON & VANDERHYE P. C.
                PRIOR APPLICATION DATA.
APPLICATION DATA.
APPLICATION DATA.
TILING DATE. 23-OC-1996
ATTORRY AGRIT TROPMATION:
NAME: INGOIA. DIAME E. 40, 027
REPERRICATION NUMBER: 40, 027
REPERRICATION NUMBER: 40, 027
REPERRICATION NUMBER: WM-02484
TELECOMMUNICATION TROPMATION:
TELECOMMUNICATION TROPMATION:
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TELECOMMUNICATION 1800MATION 1800MATION 1800MATION 1800MATION 1800MATION 1800 MATION 1800MATION 1800MAT
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STREET 1100 NORTH GLEBE ROAD, STH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: cher nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET WIMBER: 1579-83
TELECOMMUNICATION INFORMATION:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8439 GACGCTGGAAGACGT 8453
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MOLECULE TYPE: DNA (genomic)
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CLASSIFICATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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US-08-374-483-6
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DB 2; Length 34382; 70;
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                                                                                                                                                                                                                                                                                                                                                      Recombinant Adenovirus and Adeno-Associated Virus, Cell Lines, and Methods of Production and Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Howson and Howson
Box 457, 321 No. 6261551ristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release 1.0 Version 1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCLASSIFYCHON: 514
PCLASSIFYCHON: 514
PRIOR APPLICATION DATA.
PREDICATION NATA.
FILING DATE. 05-40N-1995
PRIOR APPLICATION DATA.
PREDICATION NATA. US 08/549,489
FILING DATE. WORDER. US 08/549,489
FILING DATE. NFORMATION:
NAME: Bak. Mary E.
NAME: Bak. Mary E.
REFERENCE/DOCKET NOWINGER. GANPOLIZIPUSA
TELEOPHONE: (215) 540-9206
TELEOPHONE: (215) 540-9206
8.3%; Score 15; DB 100.0%; Pred. No. 70; ive 0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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8.3%; Score 15;
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION James M. APPLICANT Files. James M. APPLICANT Files. Kersha J. APPLICANT Files. Kersha J. APPLICANT Files. Kersha J. APPLICANT Files. M. ASSOCIATED FILES OF INVENTION Recondition of TITLE OF INVENTION Merch Files. M. MADRESSEE: Howson and Howson
                                                                                                                                                                                                                                    Sequence 3, Application US/08973334 Patent No. 6261551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
                                                                                                                              7859 GACGCTGGAAGACGT 7873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 35408 base pairs
TYPE: nucleic acid
                                                                                    21 GACGCTGGAAGACGT 35
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                                           15; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Gaps
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                                                                                     COMPUTER: 128 PC COMPATIBLE
COMPUTER: 128 PC COMPATIBLE
SOFTWARE: PARENTE PC-DOS/80-DOS
SOFTWARE: PARENTE PC-DOS/80-DOS
SOFTWARE: PARENTE PC-DOS/80-DOS
SOFTWARE: PARENTE PC-DOS/80-SOS
SOFTWARE: PARENTE PC-DOS/80-SOS
CLASSIFICATION NUMBER: US/08/549,489
FILING DATE:
CLASSIFICATION NUMBER: US/08/549,489
FILING DATE:
CLASSIFICATION NUMBER: US/08/462,014
FILING DATE:
APPLICATION NUMBER: US/80/620-SOS
SOFTWARE BAX, MAY E.
NAME: BAX, MAY E.
REFERRACE/DOCKET NUMBER: 30-SOS
TELEDRANTICATION NUMBER: 31-SOS
SOFTWARE POS/80-SOS
INFORMATION POR SEQ ID NO: 31-SOSUBNEC PLARACTERISTICS:
LEWISH: 34-40 base pairs
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APPLICANT: Amalitano, Addrea
APPLICANT: Mauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Manar-Singh, Rajendra
TITLE DE LO LITTLE HATTION: IMPROVED APROVINGS VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.3%; Score 15; DB
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08735609
; Patent No. 5955360
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NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UNTELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GACGCTGGAAGACGT 35
                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen &
                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: no; MOLECULE TYPE:
US-08-549-489-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                        MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
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Perent No. 63401010
GENERAL INFORMATION
TITROGRATION
APPLICANT: Wilson, James M. APPLICANT: Go. GLANG-PING
TITLE OF INVENTION: No. 681010el Adenovirus Gene Therapy Vehicle INTEL OF INVENTION: and Cell Line
NUMBER OF SUGURNES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%; Score 15; DB 4; Length 35408; 100.0%; Pred, No. 70; tive 0; Mismatches 0; Indels
                                                                                                            Gao. Guang-Ping
TITLE OF INVENTION Recombinant Adenovirus and Adeno-
                                                                                                                                                                                                  Associated Virus, Cell Lines,
Methods of Production and Use
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Box 457, 31 No. 6270996ristown Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.0 Version 1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: -(Unicours)
APPLICATION WINNER: US 08/549,489
FILING DATE: -27-CCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAY, MARY B:
REGISTRATION WINNER: 1,1215
REGISTRATION WOMER: 1,1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 No. 6281010ristown Road
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/563,869A
FILING DATE: 03-May-2000
CLASSIFICATION: <a href="https://doi.org/10.100/">doi.org/10.100/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/973,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
    tent No. as.v.o.
GENERAL INFORMATION:
APPLICANT: Wilson, James M.
Fisher, Krishna J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35408 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                 Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19477
COMPUTER READABLE FORM:
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
, Patent No. 6270996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PA
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US-08-549-489-3
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US-08-379-452-43
                                           US-08-379-452-43
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US-09-315-372-1
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100.0%; Pred. No. 70;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hauser, Michael A.
Kumar-Singh, Rad-fendra
Murisan-O'Connor, Dennis J.
TITLE OF INVENTION IMPROVED ADENOVIRUS VECTORS
UNMERR OF SEQUENCES. 115
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENCY INFORMATION:

NAME: INGOLIA: Diane

REGISTRATION NUMBER: 40,027

REGISTRANCE/COCKET NUMBER: 40,027

TELEPRONCE/COCKET NUMBER: 40,026

TELEPRONCE/COCKET NUMBER: 40,026

TELEPRONCE/COCKET NUMBER: 40,026

TELEPRONCE/COCKET NUMBER: 40,026

INFORMATION: 1: 1: 1.
                                                                                                                                                                                                                                                      Mismatches
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APPLICATION NUMBER: 02/08/735,609
FILING DATE: 23-06-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States Of America ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                             Query Match

8.3%; Score 15;
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chamberlain, Jeffrey S. Amalfitano, Andrea
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         6936 GACGCTGGAAGACGT 6950
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STATE: California
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCYTH: 15915 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GACGCTGGAAGACGT 35
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Best Local Similarity
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Sequence 43, Application US/08379452
Fatent No. 6040174
GENERAL INFORMATION:
APPLICANT: MIGHTALION
APPLICANT: METHALI, Majid
APPLICANT: RAITRAIN, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
TITLE OF INVENTION: COMPLEMENTATION LINES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 35935;
70;
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                                                                                                                                                                                                                                                                                                                                                                                219: 22314-2736 Junes

COMPUTER READALE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: 1BM PC Compatible

OPENATING SYSTEM: PC-DGS/MS-DG

OPENATING SYSTEM: PC-DGS/MS-DG

OPENATING SYSTEM: BC-DGS/MS-DG

CURRENT APPLICATION NATA:

FILING DATE: 26-JM-1995

CLASSIFICATION: 315
                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: 1737 King Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Medlen & Carroll, LLP
F: 220 Montgomery Street, Suite 2200
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Amalficiano, Andread APPLICANT: Hauser, Michael A. APPLICANT: Hauser, Michael A. APPLICANT: Wamar-Singh, Radendra A. APPLICANT: Harrison O'Connot, Danovirus Grandle Control of Internation of INTERNATION: IMPROVED ADENOVIRUS VERNINGS CONTRESCONDENCE ADDRESSE: Mediam & Carroll, LLP GREEF: 220 Montgomery Street, Sulte 2200 STREET: 220 Montgomery Street, Sulte 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.04; Pred. No. 70; Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR94/00624
PLING DATE: APPLICATION DATA: FR 91 06482
PRIOR APPLICATION DATA: FR 91 06482
FILING DATE: S = WMY-1993
ATTORNEY/AGENT INFORMATION:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           029395-002
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APPLICANT: Chamberlain, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09315372
Patent No. 6057158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dadio, Susan M. REGISTRATION NUMBER: 40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0 INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6936 GACGCTGGAAGACGT 6950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GACGCTGGAAGACGT 35
                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                              CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                                                                                                                                                                                                                                          ADDRESSEE:
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Query Match 8.3%; Score 15; DB 3; Length 35935; Best Local Similarity 10.0%; Pred. No. 70; Matches 15; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READMBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ApplicANT: Chamberlain, Jeffrey S.
ApplicANT: Malitano, Andrea
ApplicANT: Malitano, Andrea
ApplicANT: Manser, Michael A.
ApplicANT: Manser, Singh, Rajandra
ApplicANT: Martigan O'Connor, Dennis J.
TILLE OF INMENTION: INTROVED ADENOVIRUS VECTORS
WOMERS OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
APPLICATION NUMBER: <B) FILING DATB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
                            UM-02484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/245,497
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other nucleic acid
/desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09245497
Patent No. 6083750
REGISTACTION WIBERS: 40.027
REFERENCE/OCCUT HIMBER: UN-O
TELECHMUNICATION INCORMINGN
TELEPHONE: (4(15) 197.8338
INPORMINGN FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: UN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6936 GACGCTGGAAGACGT 6950
                                                                                                                                                           LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GACGCTGGAAGACGT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 35935 base pairs
nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                US-09-244-752-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CENGTH:
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100.0%; Pred. No. 70;
cive 0; Mismatches 0; Indels
                                                                  MEDIUM TYPE: Ploppy disk
COMPUTE: IBM PC Comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIN.
APPLICATION NUMBER: US/09/315,372
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WEDING TYRE: FILAPPY disk
COMPUTER: IBN PC COMPAILELS
COMPUTER: PROSONS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRAT APPLICATION DAYA:
APPLICATION NOWBER: US/09/244,752
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ApplicATT: Chamberlain, Addres
ApplicATT: Manaer High, Addres
ApplicATT: Manaer Singh, Majendar
ApplicATT: Manaer Singh, Majendar
ApplicATT: Marcigan-Oconno, Dennis J.
MITTER SINGHATON
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STREET: 220 Montgomery Street, Suite 2200
GTY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Ingolia Diane B.
REGISTRATION NUMBER: 40,027
REPRENCE/DOCKTN NUMBER: UM-02464
TELECOMMUNICATION INFORMATION:
   United States Of America
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States Of America
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// DESCRIPTION: /desc = "DNA"
US-09-115-372-1
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APPLICATION NUMBER: 08/735,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    # Sequence 1, Application US/09244752 | Patent No. 6063622 | GENERAL INFORMATION | APPLICANT: Chamberlain, Jeffrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100./
Matches 15; Conservative
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                                               COMPUTER READABLE FORM
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                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                FILING DATE:
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      COUNTRY:
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Kumar-Singh, Rajendra

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US-09-562-919-1
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                                    Gaps
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APPLICANT: MEHTALI, Majid
APPLICANT: MEHTALI, Majid
APPLICANT: BAUTRANI Andrea
APPLICANT: BAUTRANI Andrea
TITLE OF INVENTION: COMPLEMENTATION LINES
NUMBER OF SEQUENCES: 43
NUMBER OF SEQUENCES: 43
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                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: 1737 King Street, Suite 500 CITY: Alexandria
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MEDIUM TYRE: REDABLE FORM:
MEDIUM TRE:
COMPUTER: IRN PC Compatible
OPERATING STREEM: PC-DOS/MS-DOS
OPERATING STREEM: PADLEMENT RELEASE #1.0, Vernion #1.30
CURRENT APPLICATION DATA:
MAPLICATION NUMBER: US/09/409,670
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                                    Mismatches
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 43, Application US/09409670 Patent No. 6133028 GENERAL INFORMATION:
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     100.04;
                                                                                                              21 GACGCTGGAAGACGT 35
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nucleic acid
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COUNTRY: United States
ZIP: 22314-2756
Best Local Similarity 100.
Matches 15; Conservative
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APPLICANT CHEM. H.
APPLICANT CHEM. H.
APPLICANT CHEM. H.
TITLE OF INVENTION METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION MADER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
CURRENT FILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-04-05
EARLIER FILING DATE: 1999-03-16
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STREET: 220 MONGAGENETY STREET, SUITE 2200

CITY: 53n Francisco

CITY: 53n Francisco

CITY: 53n Francisco

CITY: 54n Francisco

COMPUTE: United States Of America

COMPUTE: BLODGY GIARS

COMPUTE: READALE FORM:

MEDIUM TYPE: PLORDY disk

COMPUTE: BRANCH SYSTEM: PC-DGS/MS-DGS

SOFTWARE: PARENTINE Relates #1.0, Version #1.30

CURRENT APPLICATION NATA:

RAPLICATION NATA:

PRIOR APPLICATION NATA:

RAPLICATION NATA:

APPLICATION N
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Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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70;
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TELECOMMUNICATION INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 705-8410
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LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ATTORNEY/AGENT INFORMATION:
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Patent No. 6342351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338
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Best Local Similarity 100.(
Matches 15; Conservative
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SEQ ID NO 7

APPLICANT: Chamberlain, Jeffrey S. Amalfitano, Andrea Hauser, Michael A.

Sequence 1, Application US/09562919 Patent No. 6451596 GENERAL INFORMATION:

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7.7%; Score 14; DB 4; Length 17;
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0; Indels
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APPLICANT: StinChocomb, Dan T.
APPLICANT: StinChocomb, Dan T.
APPLICANT: Escobedo, Jain
APPLICANT: Escobedo, Jain
APPLICANT: Escobedo, Jain
TITLE OF INVENTION: TREATWENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
MINGER OF SEQUENCES: 8502
CORRESSONDENCE ADDRESS:
      OF VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071_2066
ZIP: 90071_2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,337
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7505, Application US/08584040
Patent No. 346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
TITLE OF INVENTION: GROWING REATOR WITH PATTOR NUMBER OF SEQUENCES. 8502. ACCRESPONDER ADDRESS!
ADDRESSEE: Lyon & Lyon & Lyon STREET: Sal Weet Pitch Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/005,974
FILING DATE: OCCODER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WATCHEY, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 995-0440
TELEFAX: (7-310
INFORMATION FOR SEQ ID NO: 75
SEQUENCE CHRANCTERISTICS:
LENGTH: 17 base pairs
TYPE: INVCLEACE acid
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Matches 14, Conservative
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COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
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STATE: California
COUNTRY: U.S.A.
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Patent No. 639976

GENERAL INCEMENTION

APPLICANT: CHEN, H.

APPLICANT: LING DATE: 1099-00-7

PRICA RPLING DATE: 1999-00-7

PRICA RPLING DATE: 1999-00-7

PRICA RPLING DATE: 1999-00-7

PRICA RPLING DATE: 1998-00-7

PRICA RPLI
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                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 8.3%; Score 15; DB 4; Length 72604; Boter Local Similarity 100.0%; Pred. No. 70; Matches 15; Conservative 0; Mismatches 15; Conservative 0; Mismatches 15; Conservative 16; Mismatches 16; Conservative 16; Mismatches 16; Conservative 17; Conservative 17; Conservative 16; Mismatches 18; Conservative 17; Conservative 16; Mismatches 16; Conservative 16; Mismatches 16; Conservative 16; Mismatches 16; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 72604; 70;
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| Paren No. 624538
| GBNERAL INFORMATION |
| APPLICANT | PAVCO, Pamela |
| APPLICANT | STINCHOOMD, Dan T |
| APPLICANT | STINCHOOMD, DAN T |
| APPLICANT | SEGUENCE, DAN T |
| APPLICANT | SEGUENCE, DAN T |
| APPLICANT | SEGUENCE, DAN T |
| TITLE OF INVENTION: TREATMENT OF DISEASE OR |
| TITLE OF INVENTION: CONSTITONS RELATED TO LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.3%; Score 15; DB
Best Local Similarity 100.0%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                      NAWE/KEY: modified base LOCATION: all n positions OTHER INFORMATION: n=a, c, g, or t US-09-268-992-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: all n positions
CTHER INFORMATION: n=a, c, g, or t
US-09-657-474-7
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ORGANISM: Homo sapiens
                                                                                      ORGANISM: Homo sapiens
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LENGTH: 72604
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                                                                                                                                       FEATURE:
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ABV06143
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                       of hits satisfying chosen parameters:
                                                                                                                            2185239 seqs, 1125999159 residues
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                                  - nucleic search, using sw model
                                                                           US-09-550-163-1_COPY_80_260
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Human secreted pro

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Human testicular a Human genomic DNA

Human reproductive

Result No.

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DNA encoding molec Human breate and o Human polymucleor! Human polymucleor! Streptococcus pneu 2,5-54(ketc.b-0-9)uco P. putida KT2440-a Arabidopsis thalia Zea mays DNA fragm Zea mays DNA fragm Sequence encoding human Sequence	Arabidopsis thalia Human cDNA sequence Drosophila metanog Staphylococcus epi Human cathepsin 18 Human CDNA for nov Streptococcus preu Chlamydia pneumoni Human bone marrow Human prosete exp Blantigen. Toxop Drosophila metanog Human bone marrow Drosophila metanog Human reticulin 80 Human zeticulin 80 Human zeticulin 80 Human zeticulin 80 Human zeticulin 80 Blantiow Educatione.	Tobacco DBS "GRNA remodi Staphylococcus and 2.6 Kbp fragment o Varicella-corer v Stephylococcus aur Human Secreted pro Gene #3301 used to Drosophila melanog Dissondium falcipe Human choka sequenc Arabidopsis indehi Human ovarian anti Human prostate exp Human prostate exp Human prostate exp	Human CDNA sequence  Human MIT-Interact  Human MIT-Interact  Human MIT-Interact  Human CDNA sequence  TOPSOEDDILL melanog  Human CDNA sequence  Sepidermidia gen  S. epidermidia gen  Human Drostate exp
AASO2046 AAF21615 AAF60558 AAF60558 AAF60558 AAF6059 AAF40105 AAF406629 AAF46629 AAF46629 AAF3828	AACC3146 AAH77051 ABL29301 ABL29301 ABL29301 AAH44629 AAH54805 AAN52307 AAN52306 AAN52306 AAN52306 AAH99912 AAH99912 AAH48917 AAH48917	AAA1190 AAS1196 AAS51796 AAN 0549 AAN 0549 AAS54531 AAA54453 AAA105409 AAA17772 AAH1445 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772 AAH17772	AAH16493 AAH16493 AAH16493 AAH16100 AAH1660 AAH1666 AAH1666 AAH1666 AAH1666 AAH1666 AAH1666 AAH1666 AAH1649
12 AA A AA A A A A A A A A A A A A A A A	22222222222222222222222222222222222222	221 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	42444444444444444444444444444444444444
1421 1465 1467 1467 1151 1151 1170 1170 1173 1173 1173			00000000000000000000000000000000000000
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                                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPe are derived from human HeLa cells. The SENPe can be used to produce a single exon microarray, which can be used for mesuring human agene expression in a sample derived from human cervical epithelial cells. By mesuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at firs, wipo.int/pub/published_pot_sequences.
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                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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ive 0; Mismatches 0
                                                                                                                                                                                                                        Claim 25; SEQ ID No 14365; 487pp; English
                                                Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI09965 standard; DNA; 372 BP
(MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-060840B.
03-AUG-2000; 2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
                                                Hanzel DK,
                                                                                                WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A 187
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186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATTGGAATGTTCTCTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory protein, wink2 wink1 Sequence is useful for producing a preceding accessing channel regulatory protein useful for in vitro or in vivo screening of agonistic or antagonistic compounds that are useful for treating diseases caused by obstrain tocassum activity, such as human cardiar arrivity which will be added a state of the protein and an asthma disheres, such as human cardiar arriving many incontinence, irritable colon, epilepsy, acceptovascular ischaemia, and autoimment disease.
                                                                                                                                                                                                                                                                                                      Novel potassium channel gene termed MinK2 encoding potassium channel regulatory protein, useful for screaming compounds that are useful for tracting diseases caused by aberrant potassium activity.
                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents the coding sequence of human potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACTITATCCAATITCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ACTITATCCAATITCACACACACGCTGGAAGACGTCTTCCGAAGGATTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGTTGTTCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 181; DB 22; Length 372; 100.0%; Pred. No. 5.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human breast cell single exon nucleic acid probe #3492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                              (UYCA-) UNIV CASE WESTERN RESERVE.
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                                                                                                                                                                                                        Brown AM;
                                                                                                                                                                                                                                                                                                                                                                                       1; Fig 9; 39pp; English
                                                                                18-AUG-2000; 2000WO-US22799
                                                                                                                          99US-0379201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                     Wible B,
                                                                                                                                                                                                                                            WPI; 2001-218424/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; cancer; ss
                                                                                                                                                                                                                                                               P-PSDB; AAU00215
     WO200114403-A1.
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                                                                                                                          20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                            01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2002
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                                                                                                                                                                                                     Ficker E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA44797:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                              The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases in the human particularly those diseases with polygenic actiology. The diseases include: breast cancer, discorders of development, inflammatory diseases of the breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; Mink2; potassium channel) cardiac arrhythmia; hypertension; ds;
angina; asthma; diabetes; tenal insufficiency, urinary innorthenner
triable colon; epilepsy, cerebrovascular ischaenia, autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formst directly from WiPo secification, but which buildshed_pct_esquences.
                                                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACTITATCCAATITCACACAGAGGCTGGAAGACGICTICCGAAGGATTITIATIACITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTITIATCCAATITICACACAGACGCTGGAAGACGICTICCGAAGGATITITIATTACTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human potassium channel regulatory protein, Mink2, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "MINK2 potassium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 181; DB 22; 100.0%; Pred. No. 5.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                            Claim 25; SEQ ID No 9956; 322pp; English.
                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS00245 standard; DNA; 372 BP.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-carcinoma tumours
                                                                                                                       Penn SG, Hanzel DK,
                                                                                                                                                           WPI; 2001-476286/51
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                                                                                                                                                                                                                        in a human breast
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  21-SEP-2000;
27-SEP-2000;
                                         04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATGGAAGTTTCTCTTTC 341
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Human, foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a single exon nucleic acid probe for nesuring human gene expression in a sample derived from human foatal measuring and angle exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples delived from human feetal liver. The present sequence is a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 ACTITATCCAATITICACACAGACGCIGGAAGACGICTICCGAAGGATITITATTACTIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATGGACAATTGGCGCCAGAACACAGCTGAGCAAGAGGCCCTCCAAGCCAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 ATGGACAATTGGCGCCAGAACACAGCTGAGCAAGAGGCCCTCCAAGCCAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probe of the invention.

The sequence date for this patent did not form part of the printed appealitation, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACTITATCCAATITCACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, gene expression, heart, microarray, vascular system, probe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 3557; 639pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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100.0%; Pred. No. 5.4e-82;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank
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                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                       2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                  30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                              2000US-0180312.
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04-OCT-2000; 2000GB-0024263.
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Matches 181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483447/52
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                                                                                          WO200157277-A2
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                                               Homo sapiens.
                                                                                                                                                                                                                                                                          30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
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                                                                                                                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 ACTITATCCAATTICACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGACAATTGGCGCCAGAACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT
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                                                                                                                                                                                                                                                                                                                                         New apatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breat. Acomprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
100.0%; Score 181; DB 22; Length 450;
Best Local Similarity 100.0%; Pred. No. 5.4e-86;
Matches 181; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3492; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human foetal liver single exon nucleic acid probe #3557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                                                                                                                                                                                       Chen W,
                                                                                                                2000US-0234687.
2000US-0236359.
                                                  2000US-0207456.
2000US-0608408.
                                                                                              2000US-0632366
                         2000US-0180312
                                                                                                                                                               2000GB-0024263
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                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                   MPI; 2001-496933/54
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                                           26-MAY-2000)
30-JUN-2000)
03-AUG-2000)
21-SEP-2000)
27-SEP-2000)
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                         04-FEB-2000;
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                                                                                                                                                                                                                                                       Penn SG,
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ATGGACAATTGGCGCCAGAACACAACAGCTGAAGAGGCCCTCCAAGCCAAAGTTGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGAGAACTICTACTATGTCATCCTGTACCTCATGGTGATGTTGGAATGTTCTCTTTC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequenced expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the disaposis and improved treatment of nervous system diseases much as Albaikary a disease, multiple sclerosis, sedizophrenia, epilepsy and eancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
brains -
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                                     numan; brain expressed exon; gene expression analysis; probe; microarray; Aliheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                  Human brain expressed single exon probe SEQ ID NO: 3499.
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                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                        2000US-0180312.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
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27-SEP-2000; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483446/52
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                                                                                                                                                                      W0200157275-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in smples derived from the human heart via informariays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system congenital heart disease. hypertension, cardiac arrhythmias and congenital heart disease. Note: The patent disease great for this patent did not form part of the printed affection, but was obtained in electronic format directly from MIPO at fip.wipo.int/pub/published_pct_gequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measuring human gene expression in a sample derived from human heart. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
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cardiovascular disease; hypertension; cardiac arrhythmia;
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100.0%; Pred. No. 5.4e-82;
ive 0; Mismatches 0;
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2000US-0608408,
2000US-0632366.
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                  congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity .vv. Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel
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                                                                                            WO200157274-A2
                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                              30-JUN-2000;
                                                       Homo sapiens
                                                                                                                                                                                                                              6-MAY-2000;
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GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTTTTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SIMP). The present sequence is one such probe. The SIMPs are derived from human Helscells The SIMPs can be used to produce a single exon microrary. Which can be used for measuring human gene expression in a sample derived from human cervical epithelial calls. By measuring gene expression, the probes are therefore useful in grading and/or sraging of disasses of the cervix, notaby cervical concer. We sequence data for this paerin did not form part of the printed specification, but was obtained in electronic form at the class specification, but was obtained in electronic form at the time was pecification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful f
analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 181; DB 22;
100.0%; Pred. No. 5.4e-82;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID No 3482; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                           Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI34911 standard; DNA; 450 BP.
                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                    2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                              30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                           2000US-0236359.
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Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
88
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488901/53
cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A 342
                                                                      WO200157278-A2
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                                    Homo sapiens.
                                                                                                                                                                                                                                                                           27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                       30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001
                                                                                                                                                                                                                                                              21-SEP-2000;
                                                                                                                                                                                     04-FEB-2000
                                                                                                                                                                                                       36-MAY-2000
                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
2 X E X E X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are detrived from genomic supernessed in the human bone marrow. They can be used to measurn gene expression in bone marrow samples, which may enable the improved disgnosis and treatment of cancers such as Imphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #3482 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACTITATCCAAITITCACACAGACGCIGGAAGACGTCTICCGAAGGAITITITATTACTIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTITATCCAATITICACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGAGAACTTCTACTATGTCATCCTGTACGTCATGGTGATGATTGGAATGTTCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATTGGAATGTTCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell;
                                 Human, bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO: 3519; 658pp + Sequence Listing; English
Human bone marrow expressed single exon probe SEQ ID NO: 3519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 181; DB 22;
100.0%; Pred. No. 5.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                             MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                           2000US-0207456.
2000US-060B408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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                                                                                                                                                                                                       2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488900/53
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                                                                                                                               MO200157276-A2
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                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 181;
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                                                                                                                                                                   09-AUG-2001
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Gaps

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The present invention tealest to movel single exon mutches card probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridies ar high stringency to a radicial expressed in the human breast on a right stringency to a radicial expressed in the human breast on contoins and prognosing diseases of the human breast, particularly those diseases with polygenic actiology in the diseases include breast cancer, disorders of development, inflammatory diseases of the preset, thorograph of the preset diseases of the breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 ACTITATCCAATITCACAGAGGCGTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTATGGAATGTTCTTTTC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGAATGTTCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACTITATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon probe from lung SEQ ID No 3487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 181; DB 22; Length 450; Ilaxity 100.0%; Pred. No. 5.46-82; Conservative 0; Mismacches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID No 3429; 322pp; English
                                                                                                                                                                                                                                                                      Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABS03496 standard; DNA; 450 BP.
                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                      Chen W,
                                                                                                                           2000US-0207456,
2000US-0608408,
2000US-0632366,
                                                                                2001WO-US00661
                                                                                                                                                                         2000US-0234687
                                                                                                                                                                                                       2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-carcinoma tumours
                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                     WPI: 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 181; Conserv
                 WO200157270-A2.
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                                                                                                                           26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                              29-JAN-2001;
                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                       04-OCT-2000;
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                                                 09-AUG-2001
                                                                                                                                                                                                                                                                      Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTTTTC 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting an arrowarsy for predicting, measuring and displaying gene expression in samples derived from human platenia. The probes are useful for artenated id signosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGACAATTGGCGCCAGAACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTITATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGACCCTCCCAAGCCAAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 181; DB 22; Length 450; Beet Local Similarity 100.0%; Pred. No. 5.4e-82. Matches 181; Conservative 0; Mismatches 0; Indels 0
Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; SEQ ID No 3597; 654pp; English.
                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멾.
                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                      2000US-0207456.
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2000US-0234687,
2000US-0236359.
                                                                                                                                                                                                                                                                  2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI03438 standard; DNA; 450
                                                                                                                                        2001WO-US00663
                                                                                                                                                                         2000US-0180312
               qenetic disorder; ss
                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                           WO200157272-A2
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                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                               Homo sapiens
                                                                                                                                        30-JAN-2001;
                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                      26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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  셤
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chronic obstructive pulmonary disease, interstitial lung disease, tuberila didopatic pulmonary fibrosis; neurofibromacosis, sucredibromacosis, cuberila didopatic pulmonary fibrosis; neurofibromacosis, sucredibromacosis, pulmonary by syndrome; astacoiddes; pulmonary haemosidarosis; pulmonary histocytosis; lymphangicleiomyamcosis; karagener syndrome; pulmonary alveolar proteinosis; Elbrocyutic pulmonary dysplasis; hydinary ciliary dyskinesis; pulmonary hypertension; hydinary ciliary dyskinesis; pulmonary hypertension;
ds; single exon probe; asthma; lung cancer; COPD; ILD
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WO200186003-A2. Нощо варіеля

15-NOV-2001

30-JAN-2001; 2001WO-US00665 04-FEB-2000; 26-MAY-2000; 30-JUN-2000;

2000US-207456P. 2000US-0608408. 2000US-0632366. 2000US-234687P. 2000US-236359P. 2000GB-0024263 -SEP-2000; 04-OCT-2000; 03-AUG-2000; 21-SEP-2000;

(MOLE-) MOLECULAR DYNAMICS INC.

Rank DR; Chen W, Hanzel DK, Penn SG,

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -

Claim 1; SEQ ID No 3487; 634pp; English.

probes. Also included are a microarray comprising the novel set of notes the novel set of probes within Mynthales at high stringsency to a nucleic card expressed in the human lung, measuring gene expression in a collection of detectably labeled muclinic acids derived from human lung, comprising of a collection of detectably labeled muclinic acids derived from human lung of man, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising of the array; identifying exons in a eukaryotic genome, comprising confine eukaryote, and (b) detecting specific hybridisation of detectably clabeled muclic acids from elearyote lung makes, to a single sen probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assiming exons to a single gene comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 The invention relates to a spatially-addressable set of single exon 

tissues and (0) measuring the expression or each or the exons in several interactions having a probe with the exon, where a common pattern of expression of the swam in the exon common pattern of expression of the swam in the tissues und/or cell types uning hybridiation to a single exon expression of the swam in the tissues und/or cell types undicates that the the exons should be assigned to a single gene a peptidic comprising one of 12011 sequences, mentioned in the spucification, or encoded by the copy probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly capital human lung derived mank, and for the study of lung disease counts as asthma. Aung cancer, chronic obttructive pulmonary disease. Cropp), interacticial lung disease (IID), familial idopathic pulmonary fibroris, neurofibronatosis, tuberous selerosis, guacher's disease, themmanky-budlak hyphrome astrocides; pulmonary plantant control of the contr probe of the invention.

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                                                                                                                                                                                                                                                           162 ACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #5189 for gene expression analysis in human cervical cell sample.
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                                                                                                                                                                                                                                                                                                                                        222 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT
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                                                                                                                                        100.0%; Score 181; DB 24; Length 450;
                   of the printed specification, but was obtained in electronic format directly from WIPO at
Note: The sequence data for this patent did not form part
                                                                                                                                                                              Indels
                                                                                               Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
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                                                                                                                                                         Pred. No. 5.4e-82;
                                                                                                                                                   100.0%; Preq. wc.
                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                            Matches 181; Conservative
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Best Local Similarity
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04-FEB-2000; 2000US-0180312. 26-MAY-2000; 2000US-0207456. 30-JAN-2001; 2001WO-US00670 WO200157278-A2 Homo sapiens 09-AUG-2001.

30-JUN-2000; 2000US-060B40B. 03-AUG-2000; 2000US-0632366. 21-SEP-2000; 2000US-02346B7. 27-SEP-2000; 2000US-0236359. 04-OCT-2000; 2000GB-0024263 (MOLE-) MOLECULAR DYNAMICS INC

Chen W, Rank DR; Hanzel DK, sg, Penn

WPI; 2001-488901/53.

Human genome-derived single exon nucleic acid probes useful f analyzing gene expression in human cervical epithelial cells Claim 25; SEQ ID No 5189; 487pp; English.

(SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used from mana gene expression in a sample derived from human cervical epithelial cells. By measuring gene The present invention relates to human single exon nucleic acid probes

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61 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
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gastric acid secretion; anti-arrhythmic agent; myocardial infarction; ss.
                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO art top wipo intr/pub/published_pot_sequences.
breast. The probes are useful for predicting, diagnosing, grading, stepling, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aeriology. The diseases include breast cancer, disorders of development, inflammatory diseases of the breast, thoroystic changes, proliferative breast disease and mon-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                  245 ACTITATCCAATITCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
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                                                                                                                                                                                                                               100.0%; Score 181; DB 22; Length 471; 100.0%; Pred. No. 5.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of human potassium channel subunit IsK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "potassium channel subunit IsK2"
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                                                                                                                                                                                           Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                        365 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGGTGGTTGGAATGTTCTCTTTC 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , breast disease; breast cancer; development disorder; ss; disease; proliferative breast disease; non-carcinoma tumour.
  expression, the probes are therefore useful in grading and/or staging off diseases of the cervix, notably cervical cancer.

Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from MIPO and to the vipo intro/pub/shubilshed_pot_eequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single exon nucleic acid probe used to measuring gene expression
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                                                                                                                                                      22; Length 471;
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                                                                                                                  Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
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                                                                                                                                                      100.0%; Score 181; DB 22; 100.0%; Pred. No. 5.4e-82;
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
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                                                                                                                                                                        Local Similarity
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26-MAY-2000;
30-JUN-2000;
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rang YT, Liu C, Drmanac RT;

2001-457740/49. P-PSDB; ABB11948

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Tevels of many expression and to isolar homologous sequences for recombinant expression of 1872; in gene therapy to increase potassium for damnel activity and to generate transgenic animals, as models and for drug screening. Recombinant 1872 is used for studying biochemical activity of 1872 and its role in disordute of gastric motility and gastric acid secretion, and to raise specific antibodies. Is a modulators are potentially useful for treating diseases associated with increased or reduced potassium channel activity e.g. as an experienced and anti-arrhythmic seques for treating myocardial infarction and as regulators of gastric acid secretion.
The present sequence encodes a human potassium channal subunit, designated 18K2. The 18K2 polyuucleotide, and detived probes, are used diagnostically to detect mutations in the 18K2 gene, to determine
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Sequence 471 BP; 143 A; 110 C; 103 G; 115 T; 0 other;

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                                                                             1 ACTITATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
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  DB 22; Length 471;
                                     Indels
100.0%; Score 181; DB 22; 100.0%; Pred. No. 5.4e-82;
                                     0; Mismatches
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ABA09192 standard; cDNA; 600 BP. 11-JAN-2002 (First entry) ABA09192; RESULT 16 ABA09192 

cytokine; cell proliferation; cell differentiation; growth factor; Human MiRP1 homologue-encoding cDNA, SEQ ID NO:968.

cell culture, drug erreening, gene therapy, antiathilametory, antiatethmatic, antiarthritis, haemostatis, antiarteriosclerotis; cytostatis, osteopathis, vasotropis, cardiant, viruside; antibacterial; antibacterial; antibacterial; santibacterial; ses. haematopoissis regulation; tissue growth, immunomodulator; scrivin, infinits chemcarats; chemchines; thrombolysis oncognessis; proliferation; metastasis; cancer; tumont; haematopoietic disorder; propoid call disorder; atthms; arthritis; chronic fillammatory condition; proliferative retinopathy; arthritis; chronic fillammatory condition; proliferative retinopathy; bone disorder; observables of sease; arterial isochaemia; bone disorder; osteoporosis, vascular growth disorder; osteoporosis, vascular growth disorder; osteoporosis, vascular growth disorder;

WO200157188-A2.

05-FEB-2001; 2001WO-US03800. 09-AUG-2001

(HYSE-) HYSEQ INC

03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

Sequences ABB10981-ABB12310 represent 1350 novel human polypeptides, and equences ABB10981-ABB12310 represent nucleic acide encoding them. The invention also relates to vectors and recombinant host cells comprising a convection also relates to vectors and recombinant host cells comprising a control also relates to vectors and recombinant host cells comprising a control also related to the invention, methods of packeting the nucleotides control and page them to the properties of the invention. Although novel, many of the bind to polypeptides of the invention and though novel, many of the control interapeutic applications. The polypeptides of the invention may giving an insight into their probable biological activities, and hence to polypeptides of the invention are lighterentiation activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activities, receptor or lighted activities, or may be commonodulatory activity; tissue growth activity; chemotactor or chemokinetic activities, haemotetic, thrombotic or control and their biological activities, propeptides and mucleotides of the invention are useful for preventing, treating or metastasis.

Conditions, e.g., by proper or lighted activities, or may be conditions in their biological activities, webload or lymphoid cell conditions in chronic inflammatory conditions from the activities or proliferative retringeatby, athereorders (e.g., actherm or arthritis), critical cauld and disorders (e.g., actherm or arthritis), critical properties are not all proliferation and disorders (e.g., actherm or arthritis), critical and disorders (e.g., actherm or arthritis), critical and disorders (e.g., actherming the many be used to promote wound to respect the many part of activities and purposed activity may be used in collutions to wind the hose with the many properties and proliferation to immune disorders to proliferation and activity may be used in activity may be used in a disorders to 120 that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions and in drug accending techniques. The present sequence represents a cobw encoding a screening techniques. The present sequence represents a cobw encoding a 44 ACTITATICCAATITICACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 103 163 9 61 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGCCCCTCCAAGCCCAAAGTTGAT 104 ATGGACAATTGGCGCCAGAACACACTGAGCGCAAGAGGCCCTCCAAGCCAAAGTTGAT 1 ACTITATCCAATITCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTIAT Gaps Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. architits and cancer -.. Length 600; Indels Sequence 600 BP; 187 A; 133 C; 130 G; 144 T; 6 other; DB 22; 100.0%; Score 181; DB 22; 100.0%; Pred. No. 5.5e-82; Best Local Similarity 100.0%; Pred. No. 5.5 Matches 181; Conservative 0; Mismatches novel human polypeptide of the invention. English. Claim 1; Page 826; 1963pp; Query Match 셤 ò 셤

A 181 181

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A 224

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encoded polypeptides (AMPN8323-AM80309) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoptides and polypeptides are useful in gene therapy. Waccines or peptide therapy. The polypeptides are various cytokine-like activities, escip, seem activity, meanstopocasis regulating activities, city, tissue growth factor activity, immunomodulatory activity and activity, insue growth factor activity, immunomodulatory activity and activity insue growth factor activity in the properties of t
   104 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 163
                                                                                                                 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, cytokine; cell proliferation, cell differentiation; gene therapy, vaccine, peptide therapy; stem cell growth factor; haematopoiceis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                         164 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the sequence listing
                                                          121 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTTGGAATGTTCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2111 (AAK52582) and 3666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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ng Zw;
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R, Wang
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Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                           AAK51661 standard; cDNA; 655 BP
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27-ARP-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0520325.
01-SBP-2000; 2000US-0554936.
11-SBP-2000; 2000US-0564551.
20-OCT-2000; 2000US-0539325.
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Wang D, 1
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Zhao QA,
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                                                                                                                                                                                                                                                                                                                    RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucloscides (AAK51455-AAK3145) and the encoded polyneptides (AAK71450-) that extibit activity elating to cytokine should in other catholication or which may induce production of other cytokines in other cath populations. The production of other cytokines in other cath populations. The polynucloscides are useful in gene therapy, vaccines or populate therapy to pypopulate have various cytokine-like activities, e.g. stem cell growth factor activity, hammingologies acquibiting activity, rissue growth factor activity, hammingologies crivity and activity and may be useful in the diagnosis and/or
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                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchine; peptide therapy; serem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; se.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTe: Records for SRO ID NO 2110 (AAK52591), 2111 (AAK52592) and 3666 (AAM8020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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R, Wang ZW;
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Wang D, Wang J, Zhang J, Ren F, Chen
ang Y, Wejhrman T, Goodrich R;
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                                                      AAK52645 standard; cDNA; 600 BP
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Yang Y, Wejhrman T,
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2000US-0598075.
2000US-0598075.
2000US-0654936.
2000US-066351.
2000US-0693325.
2000US-0693325.
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Matches 181; Conservative 0
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19-JUL-2000;
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20-OCT-2000;
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Zhao QA,
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long Gor syndrome; LOFT; single nucleotide polymorphism; cardiac arrythmia;
pocassium channel; se; gene.
nonhaman animals comprising a heterologous ion channel protein genee of the invention, a transcent calman football and RECE2 and HERG DNA, and methods of and exceeding druge for treating long Or syndrome NNA, and methods of and exceeding druge for treating long Or syndrome and antibodis or sections of the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 ACTITATCCAATITCACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
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                                                                                                                                                                                                                                                                                                                 DB 21; Length 732;
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                                                                                                                                                                                                                                                                                                             100.0%; Score 181; DB 21;
100.0%; Pred. No. 5.5e-82;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                      61 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, KCNE2; MiRPI; potassium channel protein; KNCE1-related;
MinK-related; long OT syndrome, cardiae arrhythmia,
drug screening; Knockou mouse; transgenic animal; ion channel disorder;
fast delayed rectifier potassium channel; anti-KNCE2 antibody;
                                                                                                                                                                      1 ACTITIATICCAATITICACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:1.
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                               Length 655;
                                                                                     Indels
                               100.0%; Score 181; DB 22; 100.0%; Pred. No. 5.5e-82;
                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 118-119; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC64071 standard; cDNA; 732 BP.
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                                                                                     Matches 181; Conservative
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                                                            Local Similarity
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                                   Query Match
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P-PSDB; AAE22094.
                                                                                                                                                        WO200222875-A2.
                                                                                                                                                                                                                                                                                                                            Goldstein SAN,
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                                                                                      variation
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                         The invention relates to identifying (M1) a compound that modulates to tolobical activity of a potassium feature (PC), by contacting a compound with a structure comprising a PC polypeptide and a polypeptide and a polypeptide and a polypeptide and a polypeptide compound with a structure comprising a PC polypeptide and a polypeptide and a polypeptide and a civity of the PC polypeptide in the presence and absence of the compound that activities indicates modulation of both operation of a compound that modulates the biological activity of a complex comprising that modulates the biological activity of a complex comprising a human ether-a-g-og-related gene (HERG) channel polypeptide and a KCRI coppeptide, identifying (M3) a candidate compound as a modulator of KCRI expression, modulating (M3) a candidate compound as a modulator of KCRI expression, modulating (M3) a candidate compound as a modulator of KCRI expression, modulating the busing (M3) a candidate compound as a modulator of KCRI expression, modulating the supplect, comprising of administering to the subject, comprising obtaining a compound as a modulator of kCRI induced cardiac arithythmia in a subject, comprising obtaining a compound that an indicate arithythmia, an oligomulectide pair, where a first princip of a modulating the confidence of the pair bybridies to a first portion of a KCRI comprising of a modulating and confidence of the pair bybridies to a second portion of a KCRI comprising a compound the modulating preference of the KCRI gene that is adjacent to the first portion and a set of anticanse confidentifying a portion of a KCRI compound a compound the modulating preference of a modulating in drug a compound the modulating a modulating in drug compound the modulating a percenting in drug presenting only syndrome (LOT) and a useful for the present properting a modulating and modulating a modulating a modulating and modulating and modulating and modulating a 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Min-K related ion channel protein; MIRP;, ion channel disorder; Wisz; long OT syndrome; LOGS; cardiao arrhythmia; mutant; gene; SNP; strigle nucleoide polymorphism; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
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Claim 17; Page 162-163; 164pp; English.
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The present invention relates to novel KCNE2 genes encoding Min-K related (MIRP) I non channel proteins and polymorphisms in these genes that are associated with lon channel disorders including antibiocric-induced long off syndrome (LQTS). Detecting a muterion at amino acid positions 8, 54, 57 or 116 of MiRPL polymeptide or a muterion at a muclecide position encoding the amino acid positions is useful for disquosing the presence of a polymorphism that causes druy-induced LQTS. The disagnostic methods are useful in the development of new drug therapies which selectively target on or more KCNE2 polymorphisms that care associated with cardiac arrhythmise. The present sequence is human KCNE2 mutent bNA (420F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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200 GCTGAGAACTTCTAATGTCATCCTGTGACCTGATGGTGATGGAATGTTCTTC 259
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                                                                                                                                                                                                      /standard name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel gene encoding Min-K related ion channel protein subunit and polymorphisms in this gene associated with antibiotic-induced long QT
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                                                                                                     "Human MiRP1 mutant protein"
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Location/Qualifiers
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                                                                                                                                 replace (420, C)
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Human KCNE2 wild type DNA

Homo sapiens

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The invention relates to novel ion channel proteins related to the invention relates to novel ion channel proteins of the five the five five file acids acids according them. The proteins of the invention are human and rack (KME2 (MRR1; AAB29585 and AAB29586, respectively); and human and mouse KCME2 (MRR1; AAB29585 and AAB29588, respectively); and human and mouse KCME2 (MRR2; AAB2958 and AAB29590, respectively); and number successing these proteins are given in AAB29590, AAB20590; respectively); and man and mouse KCME4 (MRR2; AAB29589 and AAB29590, respectively); and part human and mouse KCME2, while are associated with long OT syndrome. The invention also relates to methode of disquesting of the combinan antimals comprising a heterologue is not channel protein agene of the invention in an endogenous KCME2, KCME3 or KCME4 gene, transgenic of intended of an arthodes of and screening drugs for treating long OT syndrome using KCME2 proteins in the methods and antipolice against KCME2 proteins. The embtods, antibodies nuclaic acids and proteins may be used for disquesting or treating ton channel of subcoders, especially long OT syndrome treating ton channel of subcoders, especially long OT syndrome (Treating or syndrome acids, and proteins may be used for disquesting or syndrome acting KCME2 protein and the sepecially long OT syndrome and the sepecially pencing the present acquence represents DNA encoding a mutant human KCME2 (MRR2) specifically claimed for use in dispussion and drug screening channels and the inventions.
                                                                     Human; KCNE2; MiRP1; potassium channel protein; KOKE1-related;
MinK-related; long CT syndrone; cardiac arrhykhmia;
drug screening; Knockout mouse; transgenic animal; ton channel disorder;
fast delayed rectifier potassium channel; anti-KNCE2 antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long QT annitroms.
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                         Human potassium channel protein KCNE2 (MiRP1) T8A mutant DNA
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100.0%; Pred. No. 7.1e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Splawski I, Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 56, Page -; 132pp; English.
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Matches 165, Conserv
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                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel KCNE2 genes encoding Min-X related (MIRP) I non channel proceshs and polymorphisms in these genes that are associated with lan channel speciels and polymorphisms in these genes that are associated with lan channel disorders including antibiocic-induced long off syndrome (LQTS). Detecting a mutation at amino acid positions 9, 54, 57 or 116 of MIRP polypeptide or a mutation at a nucleotide position encoding the amino acid positions is useful for diagnosing the presence of a polymorphism that causes drug-induced LQTS. The diagnositic methods are useful in the development of new drug therapies which selectively range on or more KCNEZ polymorphisms there are associated with cardiac riphythmise. The present sequence is human KCNEZ wild type DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 ACTITIATCCAATTICACACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTCTTTC 180
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                         Human; Min-K related ion channel protein; MiRPl; ion channel disorder;
KCNE2; long QT syndrome; LQTS; cardiac urrhythmia; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel gene encoding Min-K related ion channel protein subunit and polymorphisms in this gene associated with antibiotic-induced long OT
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Pred. No. 5.5e-82;
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                                                                                                                                                                                                                                            /product= "Human MiRP1 protein"
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                                                                                                                                                            ocation/Qualifiers
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Matches 181; Conservative
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P-PSDB; AAE22095.
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                                                                                                             Homo sapiens
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The invention relates to novel ion channel proceins related to the invention relates to novel ion channel proceins related to the CRCE (MINIX) and to nucleic acids encoding them. The proteins of proteins of the invention are human and mouse KCME2 (MIRE); AAB29585 and AAB29586, respectively); human and mouse KCME3 (MIRE); AAB29585 and AAB29586, respectively); the cDNAs encoding these proteins are given in AAB29580, to respectively); the cDNAs encoding these proteins are given in AAB29590, to respectively); the cDNAs encoding these proteins are given in AAB29590, to respectively); the cDNAs encoding these proteins are given in AAB29590, to respectively); the cDNAs encoding these proteins are given in AAB29590, and AAB29590, to relate a to methods of disgnosting of the strength of the sing the KCME2, KCME3 or KCME3 or KCME3 gene, transgenic of disruption in an endogenous KCME2, KCME3 or KCME3 or KCME3 gene, transgenic of the invention, a transgenic animal comprising a transgenic animal comprising a transgenic animal comprising and the top of the invention, and antibodies against KCME2 proteins. The embtods a nucleic acids, and proteins may be used for disgnosting or treating ion channel of kCME2 and HERC are appecially long or syndrome transgenic animal comprising KCME2 proteins. The embtods a nucleic acids and surbodies against KCME2 proteins. The embtods and surbodies (for the present emptods and the surbodies and the surposition and the surpo
Human, KCNE2; MiRPI; potassium channel protein; KNCE1-related;
MinK-rebted; long QT syndrown, cardiaca arrhythmia;
drug screening; knockout mouse; transgenic animal; ion channel disorder;
fast delayed rectifier potassium channel; anti-KNCE2 antibody;
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derived from the wild-type human KNCE2 cDNA sequence shown on page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long OT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Human potassium channel protein KCNE2 (MiRP1) I57T mutant DNA.
                                                                                                                   216 ATGTCATCCTGTACCTCATGGTGATGATGAATGTTCTCTTTCA 260
                                                                                  137 ATGTCATCCTGTACCTCATGGTGATGGTTGGAATGTTCTCTTTCA
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                                                                                                                                                                                                                                                                        AAC64085 standard; DNA; 732 BP
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(UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                             AAC64085;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Min.K related ion channel protein; MIRP; ion channel disorder; KKNB2; long OT syndrome; LOTS; cardiac arrhythmia; mutant; gene; SNP; single nuclecide polymorphism; de.
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                          137 ATGTCATCCTGTACCTCATGGTGATTGGAATGTTCTCTTTCA
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100.0%; Pred. No. 7.1e-74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                             Human KCNE2 mutant DNA (A95G)
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                                                                                                                                                                                                                                                                     AAD35173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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8 8 8

139

09

Local Similarity

Query Match

118-119

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Matches 163;

80 61 140

셤 ò 유 ð

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61 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCCAAAGTTGAT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel ion channel proceins related to ROKEI (Winth) and to nuclaic so die encoding them The proceins of the first had to nuclaic so and a second the first habsysss and AABSSSS, trespectively) human and mouse (RNE3 (WIRRI) AABSSSSS and AABSSSSS, respectively). The choke smoothing these proceins are given in AACS401 AACS4016. AACS4016. AACS4016. AACS4016. ROKEIN AACS4016. AACS4016. The proceins are given in AACS4016. The processing the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mink-related; long QT syndrome; cardiac arthythmia;
drug screening, knockott mouse; transgenic animal; ion channel disorder;
fast delayed recrifier potassium channel; anti-KWCE2 antibody;
are useful in the development of new drug therapies which selectively target one or more KNB2 Pollymorphisms that are associated with cardiac arthythmias. The present sequence is human KORE2 mutant DNA (T24C).
                                                                                                                                                                                                                                                                                                                                                                                      80 ACTITATCCAATITICACACACACACACACACACCTCTCCCAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                            1 ACTITIATICCAATITICACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; KCNE2; MiRP1; potassium channel protein; KNCE1-related;
                                                                                                                                                                                               Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human potassium channel protein KCNE2 (MiRP1) Q9E mutant
                                                                                                                                                                                                                                                             Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 242
                                                                                                                            Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                           Score 163; DB 24;
Pred. No. 7.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keating MT,
                                                                                                                                                                                           Query Match 90.1%; Score 163; DB Sest Local Similarity 100.0%; Pred. No. 7.3 Matches 163; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Splawski I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 56; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-2000; 2000WO-US10004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0129404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC64083 standard; DNA; 732
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(UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-672747/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERG; mutant; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB29593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200063434-A1.
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                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                            ACTITIATCCAATITICACACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTTATTACTTAT 139
                                                                                                                                                                                                                                                                                                                                                                                               ATGGACAATTGGCGCCAGAACACAGCTAJAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAGTTGAT 199
                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, Min-K related ion channel procein; MiRPI; ion channel disorder;
KCNE2, long Of syndrome, Loffs; cardiac arrhythmia; mutant; gene; SNP;
single nucleocide polymorphism; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace (243, T)
// Crada name "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b
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                                                                                                                                     Length 732;
                                                                                                                                                                                                   IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product= "Human MiRP1 mutant protein"
                                                                       Seguence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
                                                                                                                                 ilarity 100.0%; Score 163; DB 21; 100.0%; Pred. No. 7.3e-73; Conservative 0; Mismatches 0;
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Location/Qualifiers

Homo sapiens

/\*tag= a

variation

11-SEP-2001, 2001WO-US28332. 11-SEP-2000; 2000US-231571P

40200222875-A2

AAD35172 standard; DNA; 732 BP

RESULT 26

200

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Human KCNE2 mutant DNA (T243C)

(first entry)

25-JUL-2002

AAD35172;

Claim 15; Page 46; 49pp; English.

syndrome

WPI; 2002-362360/39.

P-PSDB; AAE22097.

UYYA ) UNIV YALE.

Goldstein SAN;

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The invention relates to novel ion channel proteins related to CKENCEI (MANK) and to nucleic acids encoding them. The proteins of the invention are human and tax (KMEZ (MANK) AAR2958 and AAR2958.

Crespectively); human and mouse KCMEZ (MARZ), AAR2958 and AAR29588, respectively); human and mouse KCMEZ (MARZ), AAR2958 and AAR29588, respectively); and human and mouse KCMEZ (MARZ), AAR2958 and AAR29589.

Crespectively); The cDNAs encoding these proteins are given in AAR2601.

AAC64076, KCMEZ, AD09 with HERG, forms cardiac fast delayed rectifier to pressule members (I-KR), mutations in which are associated with long OT Syndrome using the KCMEZ, AD09 with MARZ (KMEZ) are kCMEZ quee, it anogenic and disquesting the KCMEZ, MARZ or KCMEZ quee, transgenic of distruption in an endogenous KCMEZ, KCMEZ or KCMEZ or KCMEZ or KCMEZ or KCMEZ and HERC COMPANIAN and methods of a reasonable contraining of the invention, a transgenic animal comprising human KQMEZ and HERC CMEX, and acreeming for treating Jong CK syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 ACTITATCCAATITCACACACACACGCGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATGGACAATTGGCGCCAGAACACACAGCTGAGCCAAGGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 199
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KCMEZ, long OT syndrome; LiGTs, cardiac arrhythmia; mutant; gene, SNP;
single nucleotide polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "Single nucleotide polymorphism (SNP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The present sequence is not shown in the specification, derived from the wild-type human KNCE2 cDNA sequence shown on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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/product= "Human MiRP1 mutant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.1%; Score 154; DB 21;
100.0%; Pred. No. 2.7e-68;
iive 0; Mismatches 0;
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                                                              Claim 56; Page -; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD35171 standard; DNA; 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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       eyndrome -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 AGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 ACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; KCNE2; MiRPI; potassium channel protein; KNCE1-related;
MinK-related; long Off syndrone, cardiac arrhythmia;
drug screening; Knockout mouse; transgenic animal; ion channel disorder;
fast delayed rectifier potassium channel; anti-KNCE2 antibody;
syndrome using the KNNE2, KCNE3 or KCNE4 genes, a knockout mouse with a disruption in an endogenous KCNE2, KCNE3 or KCNE4 gene, transgenic nonhuman animals comprising a heterologous ion channel procein gene of the invention, a transgenic animal comprising human facts and HERG DNA, and methods of and screening drugs for treating long OT syndrome using KCNE2 proceins (including mutants) nucleic acids encoding them and antibodies against KNCE2 proceins. The methods, antibodies, uncleic acids encoding them dialogues and proceins may be used for diagnosing or treating ion channel disorders, especially long CT syndrome. Transgenic animals comprising KCNE2 and HERG are useful for testing anti-long OT syndrome drugs.
                                                                                                                                                                                                                                                                                 The present sequence represents DNA encoding a mutant human KCNZ2 (MIRMI) specifically claimed for use in diagnostic and drug screening methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTATAGGACAATTGGCGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                           but is
                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification, but i
derived from the wild-type human RNCE2 cDNA sequence shown on page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldstein SAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human potassium channel protein KCNE2 (MiRP1) MS4T mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCCTGTACCTCATGGTGATGGTTGGAATGTTCTCTTTCA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 TCATCCTGTACCTCATGGTGATGGTTGGAATGTTCTCTTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 732 BP; 221 A; 151 C; 158 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 89.5%; Score 162; DB 21; Best Local Similarity 100.0%; Pred. No. 2.4e-72; Best Enches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Splawski I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC64084 standard; DNA; 732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-2000; 2000WO-US10004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0129404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UTAH ) UNIV UTAH RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672747/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYYA ) UNIV YALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB29594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERG; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200063434-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC64084;
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nucleit acid probes for measuring gene expression in a sample derived from human breast and #17 cells. The method involves contecting the probes with a collection of detectably labelled nucleic acids the probes with a collection of detectably labelled nucleic acids the probes with a collection of detectably labelled nucleic acids bound to each probe of the microarray. The probes are useful for bound to each probe of the microarray of probes are useful for concede proteins. They are useful for gene discovery, and for encode proteins. They are useful for seesaing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical capture for production of the involvention predisposition and/or prognosing the toxicity of chemical captures for measuring gene expression, with far less bias training the action and the production of functional information from genomic sequence. The respective of the involvention research sequence is a single exon nucleic acid probe of the invention. Proceeding the sequence of the invention or procession, which is a contraction of the invention.

**Contraction of the properties of the invention or procession in the contraction of the invention. The procession is a single with the procession and the procession with the procession and the procession with the procession and the procession ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTATTACTTATAGGCCAAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITIATIACTIATAGEGACAATIGGCGCCAGAACACAGCAGCGGAGGAGGGCCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                            New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134; DB 22; Length 312;
Pred. No. 3.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 8633; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #16161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prec. ...
                                                                                                                                                                                                                                                              Rank DR
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                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                              Chen W,
                        2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456
                                                                                                                                             04-OCT-2000; 2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134; Conservative
                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sest Local Similarity
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                            30-JUN-2000;
03-AUG-2000;
                                                                                    21-SEP-2000;
27-SEP-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
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                                                                                                                                                                                                                                                                  Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA6785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel KCNE2 genes encoding Min-K related (MIRP) I non channel proteins and polymorphisms in these genes that are associated with ion channel proteins and polymorphisms. In these genes that are associated with ion channel disorders including antibiotic-induced long off syndrome (LOTS). Detecting a mutation at amino acid positions 8, 54, 57 or 116 of MiRPI polypeptide or a mutation at a nucleotide position encoding the amino acid positions is useful for disagnosing the presence of a polymorphism that causes drug-induced LOTS. The diagnostic methods are useful in the development of new drug therapies which selectively arage one or more KCNE2 polymorphisms that are associated with cardiac arrhychmisms. The present sequence is human KCNE2 mutant DNA (77340).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 ACTITATCCAATITCACACACACGCTGGAAGACGTCTTCCGAAGGAITTTTATTACTTAT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATGGACAATTGGCGCCAGAACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACTITATCCAATITICACACACACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel gene encoding Min-K related ion channel protein subunit and polymorphisms in this gene associated with antibiotic-induced long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85:1%; Score 154; DB 24; Length 732; 100.0%; Pred. No. 2.7e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cell single exon nucleic acid probe #8633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 732 BP; 221 A; 153 C; 157 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGAGAACTTCTACTATGTCATCCTGTACCTCA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGAACTICTACTATGTCATCCTGTACCTCA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 44-45; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA49938 standard; DNA; 312 BP
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                                                                                                                     11-SEP-2001; 2001WO-US28332.
                                                                                                                                                                                 11-SEP-2000; 2000US-231571P.
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                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-362360/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                  (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAE22096
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    WO200222875-A2
                                                                                                                                                                                                                                                                                               Goldstein SAN;
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                                                                21-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TITIATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO: 16255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%; Score 134; DB 22; 100.0%; Pred. No. 3.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; SEQ ID No 13379; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK16264 standard; DNA; 312 BP
                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                               2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234587.
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                                             2000US-0180312
                                                                                                                                                                                                                                      2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AATGTTCTCTTTCA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                    04-FEB-2000; 2
26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                      04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measuring human gene expression in a sample derived from human foetal liver. The single exon mucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human petal liver. The present sequence is a single exon nucleic acid human pool of the invention.

Note: The sequence data for this parent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at [fp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITIATIACITATATGGACAATIGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TITITATTACTIATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%; Score 134; DB 22; Length 312; 100.0%; Pred, No. 3.6e-58; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 16161; 639pp + sequence listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                              04-FEB-2000; 2000uS-0180;12.

26-MYY-2000; 2000uS-020456.

30-UN-2000; 2000uS-060408.

21-SEP-2000; 2000uS-0234687.

21-SEP-2000; 2000uS-0234687.

94-0CT-2000; 2000uS-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
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                                                               30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-483447/52
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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 32
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                 Hanzel DK,
                                                                      WPI; 2001-488900/53
                                                                                                                                                                                                                                             Local Similarity
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                   Query Match
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                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
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                                                                                                                                                                                                              probes which are derived from genomic inequence expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may emble the diagnosis and improved treatment of nervous spreem diseases much as Alfahemer of disease, multiple sclerosis, and extraophemia, epiteppy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                               48 TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA 107
                                                                                                                                                                                                                                                                                                                                                                                      108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                 TITIAITACTIAIATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCA 60
                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone marrow expressed exon; genn expression analysis; probe;
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                  Example 4; SEQ ID NO: 16255; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone marrow expressed single exon probe SEQ ID NO: 16565
                                                                                                                                                                                                                                                                                                      74.0%; Score 134; DB 22; Length 312; 100.0%; Pred. No. 3.6e-58; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; cancer; leukaemia; lymphomn; myeloma; ss
                                                                                                                                                                                                                                                                                    Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                              Rank DR
                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                     2000US-0207456.
2000US-0608408.
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           2000US-0180312
                                        2000US-0632366.
2000US-0234687.
                                                            27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100. Matches 134; Conservative
                                                                                                              Hanzel DK,
                                                                                                                               WPI; 2001-483446/52
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                   26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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           04-FEB-2000;
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                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
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The present invention provides a number of single exon nuclaic acid probes which are derived from genomic sequences expressed in the human born marrow. They can be used to messure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as Tympkoms, leukaemia and mysloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA
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                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 16565; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 134; DB 22; Length 312; 100.0%; Pred. No. 3.6e-58; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other
                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
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                                                            Chen W, Rank DR
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(MOLE-) MOLECULAR DYNAMICS INC
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234359.
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human
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                                                                        The present invention relates to single exon muclaic acid probes (SENP). The present sequence is one such probe. The probes are useful for exoducting a microarray for predicting, measuring and displaying gene expression in samples derived from himm placents. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                                                                                                                                                         48 ITTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCA
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                                                                                                                                                                                                                                Length 312;
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                                                                                                                                                                                                                                              Pred. No. 3.6e-58;
                                                                                                                                                                                                                              74.0%; Score 134; DB 22;
analyzing gene expression in human placenta
                                                                                                                                                                                                                                         100.0%; Pred. No.
                                  Claim 25; SEQ ID No 16761; 654pp; English.
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2000US-0608408.
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                                                                                                                                                                                                                                                                      Matches 134; Conservative
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                                                                                                                                                                                                                                                   Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
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                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGTTGG 120
                                                                                                                        The present invention relates to human single exon nucleic acid probes (CRBN). The present equance is one south probe. The SBNs are at derived from human hear than cells. The SBNs can be used for measuring human gene expression in a sample element from human error for measuring human gene expression in a sample element from human cervical epithelial cells. The measuring sene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical canner.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms directly from MIPO
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                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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                                                                                                                                                                                                                                                                                                                                                                                      Length 312;
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                                                                                                                                                                                                                                                                                                                                            Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 74.0%; Score 134; DB 22;
100.0%; Pred. No. 3.6e-58;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                        Claim 25; SEQ ID No 12706; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207455.
30-JUN-2000; 2000US-0608408.
31-JUN-2000; 2000US-053365.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                    74.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 36
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Human genome-derived single exon nucleic acid probes useful for

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The invention relates to a spatially-addressable set of single exon tructed and probes for mesauring spen expression in a sample derived from the an inprobes for mesauring spen expression in a sample derived from the interpretation of the specification, or their complements of the 12397 open reading frames derived from the 1564 probes. Also included are a microstry comprising the movel set of probes which they from the 1564 probes included are a microstry comprising the novel set of probes which they from the sample derived from the sample derived from the sample derived from the annual trug, meaning spen expression in a sample derived from them human lung mann, and the meaning the sample detectably bound to each probe of the sample derived from them they facility and excens in a twistypic spenome, comprising the array facility and excens in a twistypic spenome, comprising the array facility predicting at least one excluded the probe in a single spen in the above medicined for excensive said (10) detectined spenicles of the probe is a findided above medicined for excensive said (10) detectined sexue probe.

In the above medicined facilities to the predicted excent probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method tise above and (b) measuring the expression of each of the exons in several tiseuses and/or cell types using hybridiation where a common pattern of expression of the exons in the issues and/or cell types indicates that the expression of the exons in the issues and/or cell types indicates that the expression of the exons in the issues and/or cell types indicates that the expression should be assigned to a single gener a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the expression analysis, and for identifying exons in a gene, particularly cusing human lung derived mRN and for the study of lung disease cush man a machina, lung disease (LD), finilial idopathic pulmonary disease.

(CODP), interestital lung disease (LD), finilial idopathic pulmonary disease, memory interestital the expression expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, kagener syndrome, librocystic pulmonary alveolar proteinosis, kagener syndrome, librocystic pulmonary dystanesis, pulmonary Mypertene and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention.

Note: The sequence data for this parent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the printed specification, but was obtained in electronic format directly from WIPO at
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Pred. No. 3.6e-58;
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                                      Claim 4; SEQ ID No 16030; 634pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 ITTIATTACTIATATGGACAATTGGCGCCAGAACACACAGCTGAGCAGAGGCCCTCCA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO aft top.wipo.int/pub/published_pot_sequences.
breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygonic actiology. The diseases include breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinom tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; Enroit cobstructive pulmonary disease; intertitial lung disease; Enroit cobstructive pulmonary disease; intertitial lung disease; tuberous sclerosis; deucher disease; Nismann-Pick disease; tuberous sclerosis; deucher disease; Nismann-Pick disease; pulmonary lasticoycless; lunghangiolehengeners prodeced pulmonary hasticoycless; lunghangiolehengeners is Karagener ayndrome; pulmonary wediar protections is forced to pulmonary and the pulmonary pulmonary pulmonary pulmonary pulmonary pulmonary pulmonary hypertends pulmonary disease; open reading frame; ORP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCGTGGTGATGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon probe ORF from lung SEQ ID No 16030.
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                                                                                                                                                                                                                                                                                                                                                  Score 134; DB 22; Length 312;
Pred. No. 3.6e-58;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                Sequence 312 BP; 94 A; 73 C; 71 G; 74 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS16039 standard; DNA; 312 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-207456P.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AATGTTCTCTTTCA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-PEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                      Query Match
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hypertension

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Gaps

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Indels

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Rat, Mink2, potassium channel; cardiac arrhythmia, hypertension; ds;
anglian aathma, diabetes, remai linufficiency; unhary inconfinence
tritleble colon; epilopsy; cerebrovascular ischaemia, autoimmune disease.
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MinK-related; Typid Typidrome, cartibie arrhythumie;
Arug screening knockout mouse; transgenic animal; ion channel disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents the coding sequence of tar potessium channel regulatory protein, Mink2 sequence is useful for producing a potessium channel regulatory protein useful for in vitro or in vivo screening of segonistic or magonistic compounds that are useful for reading diseases caused by aberrant processium activity, such as human cardiac arthythms whypercension, and man although with a human insufficiency, withaty incontinence, irritable colon, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel potassium channel gene termed MinK2 encoding potassium channel regulatory protein, useful for screening compounds that are useful for treating diseases caused by aberrant potassium activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat potassium channel protein KCNE2 (MiRP1) cDNA, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.4%; Score 26; DB 22; Length 372;
100.0%; Pred. No. 0.0021;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                    /*tag= a
/product= "MINK2 potassium channel protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebrovascular ischaemia, and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 372 BP; 95 A; 98 C; 105 G; 74 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 Greatecreracereargargar 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 GTCATCCTGTACCTCATGGTGATGAT 164
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCA-) UNIV CASE WESTERN RESERVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC64072 standard; cDNA; 468
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0379201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wible B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-218424/22.
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Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAS00216.
                                                                                                                                                                                                                                                                            WO200114403-A1.
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                                                                                                                                                                                                                                                                                                                                                                       18-AUG-2000;
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                                                                                                                                                                                                                                                                                                                           01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ficker E,
                                                                                                  Rattue sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC64072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC64072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes oligonucleotide libraries for detecting managesenger RMAs that populate a (sub-) transcribone, where the messenger RMAs that populate a genome The library comprises messenger RMAs transcribed from multiple to transcribid con units that populate a genome The library comprises are of several oligonucleotides, each capable of hybridising selectively to a set of messenger RMAs transcribed from a given transcription unit of the oligonucleotide inhering from a given transcription unit of the persone, which encodes one or more messenger RMA splice variants. Of the oligonucleotide libraries are useful for a given transcription unit of the oligonucleotide libraries on a seful of detecting mRMAs transcriptes and splice variants of human or animal content transcriptions. The libraries may also be used as specialised minimal transcriptions of detection of tissue wide a sub-transcription unit of tissue of detect transcriptions of detection of tissue, and special specific pathological series only expressed in specific tissue under a specific pathological condition; to detect developmental specific pathological condition; to detect developmental specific genes and no detect RMA cranscriptions and splice variants of a transcriptions of a pathological condition; to detect developmental specific appress and police variants of a transcription of a pathological condition; to detect the present invention in the exemplification of the present invention format disorder and condition, but was obtained in electronic format disorder invention in the present invention format directly from MIPO and the present invention of the printed condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New oligomuclectide libraries comprising oligomuclectides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for deceting tissue, pathology, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Human, mouse, rat, splice transcript, detection; RNA transcript,
splice variant, transcriptome, oligonucleotide library, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 65; 0.002;
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                                                                                                                                                                                                                                                                                                                                                                                               Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65 BP; 11 A; 18 C; 15 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                               Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.4%; Sco.
100.0%; Pred. No. v...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID 1989; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Mintz B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 벎
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental-specific genes
                                                                                                                                                                                                                     20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                     28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
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                                                                                                                                                                                                                                                                                                                                                                                           Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Conservative
                                                                                                                                                                                                                                                                                                                                            COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 26: Conserv
                                                                          Rattus norvegicus
                                                                                                                      WO200210449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LO-MAY-2001
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14-APR-2000; 2000WO-US10004.

99US-0129404.

15-APR-1999;

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Splawski I,

Sesti F,

Abbott GW,

WPI; 2000-672747/65. P-PSDB; AAB29586

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The invention relates to novel ion channel proceins related to the invention relates to novel ion channel proceins related to the invention are human and rat KORE2 (MiRFI, AAB29565 and AAB29566.

The invention are human and mouse KCRE3 (MiRFI, AAB29565 and AAB29566, respectively); human and mouse KCRE3 (MiRFI, AAB29568 and AAB29569, respectively); and human and mouse KCRE4 (MiRFI); AAB29569 and AAB29569, respectively); and human and mouse KCRE4 (MiRFI); AAB29599 and AAB29590, respectively); the cDNAs encoding these proceins are associated with long processium channels (I-KR), mutations in which are associated with long of syndrome. The invention also relates to methods of disquesing of syndrome using the KCNE2, KCNE3 or KCNE4 gene, transpersic continuant animals comprising a herecologous ion channel procein group of the invention, a transpent animal comprising them an endogenous KCNE2, KCNE3 or KCNE4 gene, transpersic control and methods of and screening drugs for treating ion channel control and antibodise against KNE2 and antibodises, nucleic caides encoding them and antibodise against KNE2 proceins. The methods, antibodise, nucleic caides, and proceins may be used for disquesing or treating ion channel control and antibodise against KNE2 and size dispussion or transpention and successing separating or transpention and successing separating and the specially long OT syndrome. Transpentic animals comprising CK reactes sequence represents a PCR primer used to amplify KNCE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCNE2, MiRP1, KCNE3, MiRP2, KCNE4, MiRP3, ion channel procedin; 
NGEL:related, MiKT-related, long OT syndrome, cardibac arrhythmia; 
KTUE1 screening; Knockout mouse; transgenic animal; SSCP analysis;
                                                                                                                                                                                              Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                  Goldstein SAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 21; Length 23;
Pred. No. 0.065;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer SEQ ID NO:14, used in KCNE2/3/4 SSCP analysis.
                                                                                                                  Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23 BP; 5 A; 4 C; 4 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GTCTTCCGAAGGATTTTTATTAC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Grerregaagarrrrrarrac 23
                                                                                                                                                                                                                                                                                  Example 1; Page 62; 132pp; English.
                                                                                                                  Splawski I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC64078 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.78:
                99US-0129404
                                                     (UYYA ) UNIV UTAH RES FOUND.
(UYYA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-2000; 2000WO-US10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
                                                                                                                  Sesti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                         WPI; 2000-672747/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200063434-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1999;
                15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-2000.
                                                                                                                     Abbott GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC64078;
                                                                                                                                                                                                                                          syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
AAC64078/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KCNE2; MiRPI, KCNE3; MiRP2; KCNE4; MiRP3; ion channel protein; 
forcil-related, winfr-related; long Of syndrome; cardiac arritylmia; 
forcil related; knockout moues; transgnil animal; SGCP analysis.
                                                                                                                                                                                                                                                           Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents cDNA encoding rat KCNE2 (MiRPI)
                                                                                                                                                         Goldstein SAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.4%; Score 26; DB 21; Length 468; Beet Local Similarity 100.0%; Pred. No. 0.0021. Marches 26; Conservative 0; Mismatches 0; Indels Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer SEQ ID NO:15, used in KCNE2/3/4 SSCP analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 468 BP; 118 A; 126 C; 131 G; 93 T; 0 other;
                                                                                                                                                            Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 GTCATCCTGTACCTCATGGTGATGAT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GTCATCCTGTACCTCATGGTGATGAT 204
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 119-120; 132pp; English.
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AAC64079 standard; DNA; 23 BP

RESULT 42 AAC64079

ò g .9-FEB-2001 (first entry)

AAC64079:

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Gaps

99US-0129404.

14-APR-2000; 2000WO-US10004.

WO200063434-A1.

26-OCT-2000

PCR primer; ss

Unidentified

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Folander K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF80272 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                     WPI; 2002-362360/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-273764/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200127246-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF80272;
                                                                                                            syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF80272
   ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                       The invention relates to novel ion channel proteins related to the five filters of the filters o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using KONEZ proteins (including minaries), nucleic acids ancoding them and antibodies against KONEZ proteins The methods antibodies nucleic acids and proteins may be used for diagnosing or treating ion channel (disorders, especially) long or syndrome franspanic animals comprising Kdisorders, especially long or syndrome franspanic animals comprising This present sequence represents a POR primer used to amplify KNCEZ, NCCEZ, and MCCEZ gene fragments for SCP analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Min-K related ion channel protein; MiRP1; ion channel disorder; KCNE2; long QT syndrome; LQTS; cardiac arrhythmia; PCR; primer; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Novel nucleic acids encoding MiRP1, MiRP2 and MiRP3, useful for diagnosing and treating ion channel disorders, especially long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                      Goldstein SAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 21; DB 21; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human KCNE2 gene amplifying forward PCR primer #2.
                                                                                      Keating MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 0.6
ive 0; Mismatches
                                                                                                                                                                                                                                                                 Example 1; Page 62; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 CTCCAAGCCAAAGTTGATGCT 123
                                                                                      Splawski I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 crccaagccaaagricargcr 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD35176 standard; DNA; 21 BP
                  (UTAH ) UNIV UTAH RES FOUND. (UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Conservative
                                                                                      Abbott GW, Sesti F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                  WPI; 2000-672747/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UYYA ) UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD35176
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The present invention relates to noval KCREZ genes encoding Min-K related MKREP 1 and themselves that to a second with the process of the pro
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Novel gene encoding Min-K related ion channel protein subunit and polymorphisms in this gene associated with antibiotic-induced long QT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; potassium channel; IsK2; gene therapy; gastric motility;
gastric acid secretion; anti-arrhythmic agent; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding the IsK2 potassium channel subunit, useful e.g. for detecting mutations and screening for therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer used to amplify potassium channel subunit IsK2 cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 21; DB 24; Length 21; 100.0%; Pred. No. 0.67; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.67;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21 BP; 4 A; 7 C; 2 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 TACTATGTCATCCTGTACCTC 153
                                                                                                                                                                          Example 1, Page 22; 49pp; English.
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US-09-550-163-1\_COPY\_80\_260

Perfect score: Scoring table:

Seguence:

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Sequence 1317, App. Sequence 18714, App. Sequence 18714, App. Sequence 18717, App. Sequence 1317, App. Sequence 1317, App. Sequence 1317, App. Sequence 2314, App. Sequence 2314, App. Sequence 2314, App. Sequence 2514, App. Sequence 11256, App. Sequence 11256, App. Sequence 11256, App. Sequence 11256, App. Sequence 1125, App.
                                                                                                                                                                                                                     Sequence 973, App
Sequence 973, App
Sequence 1636, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 157, App
Sequence 583, App
Sequence 464, App
Sequence 20062, A
Sequence 11763, A
                                                                                                                                                                                                                                                                                                        Sequence 3421, Ap
Sequence 3875, Ap
Sequence 71, Appl
Sequence 3, Appli
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Sequence 700, App
Sequence 220, App
Sequence 2, Appli
                                                                                                                                                               498, App
569, App
35, Appl

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19038, A
Sequence 19234, A
Sequence 2236, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equence 1, Appli
Sequence 4378, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Aprilance 9, P
                                                                                                                                                                                        Sequence 56
Sequence 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9
Sequence 1,
                                                                                               Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
0 US-09-864-761-3287
0 US-09-864-761-2506
0 US-09-783-590-4657
US-09-738-626-564
0 US-09-918-995-26895
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US. 09.864.761.8868

US-0.09.796.622.81.78

US-0.09.864.761.6528

US-0.09.864.754

US-0.09.864.754

US-0.09.864.754

US-0.09.864.754

US-0.09.864.60

US-0.09.86.60

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US-09-815-242-4378
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US-09-922-501-9
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US-10-198-846-2479 Sequence 2475 US-10-198-846-2174 Sequence 2174 US-10-199-846-4454 Sequence 4454 US-10-199-846-6454 Sequence 4454 US-10-198-846-6083 Sequence 6031 US-10-198-846-5108 Sequence 6031 US-10-198-846-3173 Sequence 5071 US-10-198-846-3473 Sequence 5101 US-10-198-846-3473 Sequence 9131 US-10-198-846-8313 Sequence 9131 US-10-198-846-8314 Sequence 9131	198-846-5052 1198-846-5045 1198-846-2837 1198-846-7115 1198-846-7115 1198-846-56 1199-846-42-8440 1199-846-42-8440	US-10-1289 146-57 US-10-1289 246-57 US-10-1289 246-57 US-10-1289 246-428 US-10-1289 246-428 US-10-1289 246-138 US-10-1289 246-1389 US-10-1289 246-1389 US-10-1289 246-1389 US-10-1289 246-1389 US-10-1289 246-1389 US-10-1289 246-1389 246-1389 246-1389 246-1389 246-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-1389 248-13	US-10-182.464.744e US-10-182.661.218 US-10-182.661.218 US-10-182.661.30 US-10-182.661.30 US-10-182.661.30 US-10-282.193.46 US-10-282.193.46 US-10-182.193.46 US-10-186.56.483.143 US-10-186.56.543.143	US-00-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-912-918-918-918-918-918-918-918-918-918-918
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893 9 US-10-198-846-2479 894 9 US-10-198-846-2114 895 9 US-10-198-846-8454 897 9 US-10-199-846-4454 899 9 US-10-198-846-4459 901 9 US-10-198-846-3108 901 9 US-10-198-846-507 902 9 US-10-198-846-507 902 9 US-10-198-846-8312	996 9 US-10-199-96-5052 992 9 US-10-199-96-5052 992 9 US-10-199-96-5284 994 9 US-10-199-96-5754 998 9 US-10-199-96-576-5 998 9 US-10-198-96-56-56 999 9 US-10-198-96-56-56	924 9 103-10-103-0-10-10-10-10-10-10-10-10-10-10-10-10-1	1001 9 US-09-815-4642-7448-1001 9 US-09-815-4642-7448-1001 9 US-09-866-60-00-218-1001 9 US-09-866-60-00-218-1001 9 US-09-866-60-00-218-1001 9 US-00-00-219-46-1001 9 US-00-00-219-46-1001 9 US-00-00-219-46-100-100-100-100-100-100-100-100-100-10	1167   10   10   10   10   10   10   10   1
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7.7 893 9 US-10-198-B46-2479 7.7 894 9 US-10-198-B46-2174 7.7 895 9 US-10-198-B46-4554 7.7 899 9 US-10-198-B46-4563 7.7 900 9 US-10-198-B46-5083 7.7 901 9 US-10-198-B46-507 7.7 902 9 US-10-198-B46-507 7.7 902 9 US-10-198-B46-877 7.7 905 9 US-10-198-B46-8352	7.7 906 9 US-01-198-846-2052 7.7 912 9 US-01-198-846-2052 7.7 912 9 US-01-198-846-2084 7.7 912 9 US-01-198-846-2084 7.7 918 9 US-01-198-846-2114 7.7 918 10 US-01-198-846-51 7.7 918 9 US-01-198-846-51 7.7 918 9 US-01-198-846-51 7.7 919 9 US-01-198-846-51	7.7 924 9 105-10-198 846-555 9 105-10-198 846-575 9 105-10-198 846-177 9 24 9 105-10-198 846-456 9 105-10-198 846-456 9 105-10-198 846-456 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-198 846-458 9 105-10-10-106 846-458 9 105-10-106 846-458 9 105-10-106 846-458 9 105-10-106 846-458 9 105-10-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-106 846-466 9 105-106 846-458 9 105-106 846-458 9 105-106 846-458 9 105-10	7.7 1001 9 US-10-152-661-218 7.7 1001 9 US-10-152-661-218 7.7 1015 9 US-00-866-060A-218 7.7 1015 9 US-00-866-06A-30 7.7 1021 9 US-00-866-06A-30 7.7 1021 9 US-00-219-143 7.7 1024 9 US-10-202-19-143 7.7 1081 9 US-10-066-543-143 7.7 1081 9 US-10-066-543-143 7.7 1082 10 US-00-978-676-482 7.7 1113 10 US-09-98-676-483 7.7 1113 10 US-09-98-676-483 7.7 1113 10 US-09-78-676-483 7.7 1113 10 US-09-78-676-483 7.7 1113 10 US-09-78-678-483	1144 10 05 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

Sequence 357, Sequence 357, Sequence 357, Sequence 357, Sequence 357,	357,	357,	നന	495,	357,	357,	357,	357,	357,	357,	m r	7 (	Sequence 357, App	7 0	2 6	7 (	357	) (		,,,,,	357,	Seguence 357, App	Sednence 357, App	357,	Sequence 357, App	Sequence 357, App	357,		7	m	Sequence 357. App	~	1	ddw '/cc apranhac	357,	Sequence 357, App	Seguence 357, App	Sequence 357, App	Sequence 357, App	Sequence 357, App	Seguence 357, App	. 22	. 7		ο.	357,	357,	357.	357.	-	7.77		27		, ,	357,	Sequence 357, App	357,	357		, ,	2	35	'n	3	5.	2, Ap	2	ח ו
9 US-10-140-860-357 9 US-10-142-417-357 9 US-10-147-500-357 9 US-10-147-502-357 9 US-10-147-515-357																9 US-10-127-848A-357					US-10-128-684A-357	US-10-128-686A-357	US-10-128-690A-357	NS-10-128-691A-357	US-10-131-819A-357	JUS-10-131-829A-357	US-10-131-836A-357	170-10-10-10-060	105-10-13/-868-35/	US-10-146-729-357	NS-10-146-791-357	115-10-147-484-357				9 US-10-147-512-357		US-10-175-735-357	US-10-123-905-357		9 US-10-124-815-357	TIS-10-125-9218-357															9 US-10-127-841A-357									US-10-230-417-357	US-10-235-767-2	US-10-121-051-357	100-100-177-01-00
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	Sequence 357, App	357,	357,	357,	357,	495,		495,	495,	357,	357,	400	4 90	257	257	495	495	357		, , ,		, , ,		357,	357,	357,	495,	405	,,,	495,	357,	357	357	, ,	,,,,,	357	357,	357,	495,		357,	357.	727	200		, ,	357,	357,	357,		157	357	357		,,,,,	125	357,	Sequence 357, App	357,	357	, ,	, , c c	357,	357.	200	,,,,,,	357,	Seguence 357, App	,,,,,
Sequence 35: Sequence 35: Sequence 35: Sequence 2, Sequence 2,	Sequence 357, Sequence 357,	Sequence 357,	Sequence 357, Sequence 357,	Sequence 357,	Sequence 357,	Sequence 495,	Sequence 495,	Sequence 495,	Sequence 495,	Sequence 357,	Sequence 357,	Seguence 495,	Sequence 495,	Seguence 357	Segmence 357	Semence 495.	Sequence 495.	Semience 357	Semience 495	Seguence 100,	sequence 495,	Sequence 357,	sednence 35/,	Sequence 357,	Sequence 357,	Sequence 357,	Sequence 495,	Semionos 405	Sednelice 495,	Sequence 495,	Seguence 357,	Seguence 357.	Company 257	'Acquestes on'	'accapience 32'	sednence 327,	Seguence 357,	Seguence 357,	Sequence 495,	Sequence 357,	Sequence 357,	Segmence 357.	Semience 357	736 90000000	deduction 22'	sednence 357,	Sequence 357,	Sequence 357,	Sequence 357,	Segmence 357.	Semience 357	Semence 357	Section 357.	Semience 357	Sequence 25.	Sequence 357,	Seguence 357,	Sequence 357,	Seguence 357,	Semiono 357	' CO DOMESTICO	'/sc acunence 35'	Seguence 357,	Segmence 357.	Comemon 357	Sequence 357,	Sequence 357,	Sequence 357,	Somione 337,
9 US-10-121-049-357 Sequence 315: 9 US-10-123-904-357 Sequence 315: 9 US-10-140-470-357 Sequence 35: 9 US-10-055-627-2 Sequence 25: 9 US-10-175-746-357 Sequence 25:	9 US-10-176-918-357 Sequence 357, 9 US-10-176-91-357 Sequence 357, 9 US-10-176-921-357 Sequence 357,	9 US-10-13/-865-35/ 9 US-10-140-474-357 Seguence 357,	9 US-10-142-431-357 Sequence 357, 9 US-10-143-114-357 Sequence 357,	9 US-10-140-002-357 Sequence 357,	9 US-10-142-419-357 Sequence 357,	9 US-09-978-191A-495 Sequence 495,	9 US-09-978-403A-495 Sequence 495, 9 US-09-978-564A-495 Semience 495	9 US-09-978-585A-495 Sequence 495,	9 US-10-017-081A-495 Sequence 495,	9 US-10-123-262-357 Sequence 357,	9 US-10-142-423-357 Sequence 357,	9 US-03-378-624-435 Sequence 435,	9 115-09-909-8131-495 Sequence 495,	9 US-10-121-050-357 Sequence 357	9 US-10-141-755-357 Semience 357	9 US-10-167-749-495 Sequence 495.	9 US-09-918-585A-495 Sequence 495.	9 US-10-143-032-357 Semience 357	9 11S-09-978-4231-495 Semience 495	9 116-10-013-0213-40E Sequence 430,	9 US-IU-UI3-92IA-495 Sequence 495,	9 US-IU-123-IU8-35/ Sequence 357,	9 US-10-123-236-35/ Sequence 35/,	9 US-10-123-261-357 Sequence 357,	9 US-10-140-921-357 Sequence 357,	9 US-10-140-928-357 Sequence 357,	9 US-09-978-193A-495 Sequence 495,	9 IIS-10-013-9298-495	9 05-10-013-323M-433	9 US-10-016-177A-495 Sequence 495,	9 US-10-121-045-357 Seguence 357,	9 US-10-123-292-357 Sequence 357.	9 TIG-10-123-903-357 Comission 257	100 000 000 000 000 000 000 000 000 000	, us in it is an in it is a contract of the co	9 US-10-124-822-35/ Sequence 35/,	9 US-10-140-925-357, Sequence 357,	9 US-10-160-498-357 Sequence 357,	9 US-09-999-830A-495 Seguence 495,	9 US-10-121-041-357 Sequence 357,	9 US-10-121-043-357 Seguence 357,	9 US-10-121-047-357 Segmence 357.	9 US-10-123-215-357 Semience 357	9 116-10-103-967-957	ייים בייים מני מייים מחור מייים	3 US-IU-IZ3-9UB-35/	9 US-10-123-909-357 Sequence 357,	9 US-10-123-910-357 Seguence 357,	9 US-10-124-813-357 Sequence 357,	9 US-10-124-817-357 Segmence 357.	9 US-10-124-824-357 Semience 357.	9 US-10-125-922-357 Segmence 357.	9 US-10-125-924-357 Segmence 357.	9 US-10-127-825A-357 Semience 357.	0 110-101-101-0008-361	9 US-10-12/-829A-35/ Sequence 35/,	9 US-10-127-835A-357 Sequence 357,	9 US-10-127-839A-357 Sequence 357,	9 US-10-127-901A-357 Sequence 357,	9 US-10-128-6938-357	100 and 101 an	3 05-10-131-813A-35/ Sequence 35/,	9 US-10-131-818A-357 Seguence 357,	9 US-10-131-823A-357 Seguence 357.	9 119-10-131-8245-257 Company 257	0 110 10 101 000% 017 000 01 01 01 01 01 01 01 01 01 01 01 01	9 US-10-131-830A-357 Sequence 357,	9 US-10-131-837A-357 Seguence 357,	9 TR-10-137-6738-357
3283 9 US-10-123-049-357 Sequence 35: 3283 9 US-10-123-904-357 Sequence 35: 3283 9 US-10-140-470-357 Sequence 35: 3283 9 US-10-130-470-357 Sequence 27: 3283 9 US-10-175-476-357 Sequence 27: 3283 9 US-10-175-476-357	3283 9 US-10-176-918-357 Sequence 357, 3283 9 US-10-176-921-357 Sequence 357, 369 US-10-176-970 Sequence 357, 369 US-10-17	3283 9 US-10-137-865-357 Sequence 357, 3283 9 US-10-140-474-357 Sequence 357,	3283 9 US-10-142-431-357 Sequence 357, 3283 9 US-10-143-114-357 Sequence 357,	3283 9 US-10-140-002-357 Sequence 357,	3283 9 US-10-142-419-357 Sequence 495,	3283 9 US-09-978-191A-495 Sequence 495,	3283 9 US-09-978-403A-495 Sequence 495, 3283 9 US-09-978-564A-495 Semience 495	3283 9 US-09-978-585A-495 Sequence 495,	3283 9 US-10-017-081A-495 Sequence 495,	3283 9 US-10-123-262-357 Sequence 357,	3283 9 US-10-142-423-357 Sequence 357,	3283 9 US-US-378-624-433 Sequence 493,	3263 9 03-09-981-913A-493 Sequence 493,	3283 9 US-10-121-050-457 Semience 459,	3283 9 US-10-141-755-357 Semience 357	3283 9 US-10-167-749-495 Semience 495.	3283 9 US-09-918-585A-495 Sequence 495,	3283 9 DS-10-143-032-357 Semience 357	3283 9 US-09-978-4238-495 Semience 495	3283 9 116-10-013-0218-40E COMMONDO 40E	2263 9 US-IU-UIS-921A-495 Sequence 495,	3263 9 US-IU-IZ3-IU8-35/	3263 9 US-10-123-236-35/	3283 9 US-10-123-261-357 Sequence 357,	3283 9 US-10-140-921-357 Sequence 357,	3283 9 US-10-140-928-357 Sequence 357,	3283 9 US-09-978-193A-495 Sequence 495,	3283 9 TR-10-013-9298-498	2202 3 US-10-013-323A-433 36Quence 435,	3283 9 US-10-016-177A-495 Sequence 495,	3283 9 US-10-121-045-357 Sequence 357,	3283 9 US-10-123-292-357 Sequence 357.	3283 9 IIC-10-123-903-357	COLOR DOLLAR DESCRIPTION OF THE COLOR OF THE	12403 Variable 2010-124-011-2010 Seducince 2010	3283 9 US-10-124-822-35/ Sequence 35/,	3283 9 US-10-140-925-357 Sequence 357,	. 3283 9 US-10-160-498-357 Seguence 357,	3283 9 US-09-999-830A-495 Seguence 495,	3283 9 US-10-121-041-357 Sequence 357,	3283 9 US-10-121-043-357 Sequence 357,	3283 9 US-10-121-047-357 Segmence 357.	3283 9 US-10-123-215-357 Semience 357	3283 9 IIC-10-123-002-257	ייייי אייייייייייייייייייייייייייייייי	102 3 102 102 103 103 103 103 103 103 103 103 103 103	3283 9 US-10-123-909-357 Sequence 357,	3283 9 US-10-123-910-357 Sequence 357,	3283 9 US-10-124-813-357 Sequence 357,	3283 9 US-10-124-817-357 Segmence 357.	3283 9 US-10-124-824-357 Semience 357	3283 9 US-10-125-922-357 Semience 357.	3283 9 US-10-125-924-357 Seguence 357,	3283 9 US-10-127-825A-357 Semience 357.	3383 9 110-101-101-0008-363 Sequence 337,	3283 9 US-10-12/-829A-35/ Sequence 35/,	3283 9 US-10-12/-835A-357 Sequence 357,	3283 9 US-10-127-839A-357 Sequence 357,	3283 9 US-10-127-901A-357 Sequence 357,	3283 9 US-10-128-693A-357 Semionre 357	100 0000000000000000000000000000000000	3283 9 US-10-131-813A-35/ Sequence 35/	3283 9 US-10-131-818A-357 Sequence 357,	3283 9 US-10-131-823A-357 Sequence 357.	3283 9 119-10-131-8248-357	3263 9 US-IO-ISI-624A-33/ Sequence 35/,	3283 9 US-10-131-830A-357 Seguence 357,	3283 9 US-10-131-837A-357 Sequence 357,	3283 9 HC-10-137-6328-253 55446HC 557,
9 US-10-121-049-357 Sequence 35: 9 US-10-123-904-357 Sequence 35: 9 US-10-140-470-357 Sequence 35: 9 US-10-055-627-257 Sequence 27: 9 US-10-175-746-357 Sequence 35:	7.7 3283 9 US-10-176-918-357 Sequence 357, 7.7 3283 9 US-10-176-918-357 Sequence 357, 7.7 3283 9 US-10-176-918-357 Sequence 357, 7.7 3283 9 US-10-176-918-357	7.7 3283 9 US-10-137-865-357 Sequence 357, 7.7 3283 9 US-10-140-474-357 Sequence 357,	7.7 3283 9 US-10-142-431-357 Sequence 357, 7.7 3283 9 US-10-143-114-357 Sequence 357,	7.7 3283 9 US-10-140-002-357 Sequence 357,	7.7 3283 9 US-10-142-419-357 Sequence 357,	7.7 3283 9 US-09-978-191A-495 Sequence 495,	7.7 3283 9 US-09-978-403A-495 Sequence 495, 7.7 3283 9 US-09-978-564A-495 Semience 495.	7.7 3283 9 US-09-978-585A-495 Sequence 495,	7.7 3283 9 US-10-017-081A-495 Sequence 495,	7.7 3283 9 US-10-123-262-357 Sequence 357,	7.7 3283 9 US-10-142-423-357 Sequence 357,	7.7 3283 9 116-08-978-828-493 Sequence 493,	7.7 3283 9 HS-09-999-8338-495 Cequence 495,	7.7 3283 9 US-10-121-050-357 Semience 357	7.7 3283 9 US-10-141-755-357 Semience 357	7.7 3283 9 US-10-167-749-495 Seguence 495.	7.7 3283 9 US-09-918-585A-495 Sequence 495,	7.7 3283 9 US-10-143-032-357 Semience 357	7.7 3283 9 US-09-978-423A-495 Semience 495	7.7 3283 9 116-10-013-0218-405 00000000000000000000000000000000000	7.7 3203 9 US-IU-UL3-92LA-495 Sequence 495,	7.7 3263 9 US-10-123-108-357 Sequence 357,	1.1. 3223 9 US-1123-236-35/ Sequence 35/,	1,1 3283 9 US-IU-IZ3-Z61-357 Sequence 357,	7.7 3283 9 US-10-140-921-357 Sequence 357,	7.7 3283 9 US-10-140-928-357 Sequence 357,	7.7 3283 9 US-09-978-193A-495 Sequence 495,	7.7 3283 9 113-10-013-9295 495 20-01-01	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	7.7 3283 9 US-10-016-177A-495 Sequence 495,	7.7 3283 9 US-10-121-045-357 Sequence 357,	7.7 3283 9 US-10-123-292-357 Sequence 357	7.7 3283 9 115-10-123-963-357	CONTRACTOR OF THE CONTRACTOR O	Step 9 US-121-121- Sequence 357,	1.1 3243 9 US-IU-IZ4-8ZZ-351 Sequence 351,	7.7 3283 9 US-10-140-925-357 Sequence 357,	7.7 .3283 9 US-10-160-498-357 Sequence 357,	7.7 3283 9 US-09-999-830A-495 Sequence 495,	7.7 3283 9 US-10-121-041-357 Sequence 357,	7.7 3283 9 US-10-121-043-357 Sequence 357,	7.7 3283 9 US-10-121-047-357 Seguence 357.	7.7 3283 9 US-10-123-215-357 Semience 357	7 7 3283 9 115-10-123-902-357	יייי שמיייי של מיייי ליייי לייייי לייייי לייייי ליייייי ליייייי	, seguence 121-121-121-121 Seguence 131	1.7 3283 9 US-10-123-909-357 Sequence 357,	7.7 3283 9 US-10-123-910-357 Sequence 357,	7.7 3283 9 US-10-124-813-357 Sequence 357,	7.7 3283 9 US-10-124-817-357 Seguence 357.	7.7 3283 9 US-10-124-824-357 Semience 357	7.7 3283 9 US-10-125-922-357 Semionce 357	7.7 3283 9 US-10-125-924-357 Sequence 357,	7.7 3283 9 US-10-127-825A-357 Semience 357	7 7 7 202 0 116-10-107-00-00-0	7.7 3283 9 US-10-127-829A-357 Sequence 357,	7.7 3283 9 US-10-127-835A-357 Sequence 357,	7.7 3283 9 US-10-127-839A-357 Sequence 357,	7.7 3283 9 US-10-127-901A-357 Sequence 357,	7.7 3283 9 US-10-128-6918-357	THE COUNTY OF TH	11. 3283 9 US-IN-I3I-813A-35/	7.7 3283 9 US-10-131-818A-357 Seguence 357,	7.7 3283 9 US-10-131-823A-357 Sequence 357.	7.7 3283 9 119-10-131-8248-357	7.7 See a usato total segmence 357,	7.7 3283 9 US-10-131-830A-357 Sequence 357,	7.7 3283 9 US-10-131-837A-357 Seguence 357,	7 7 3283 6 HG-101-27-60/08-369 Dominance 357,

4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ance 347, App ance 347, App	347,	347,	347,	347,	347,	74.	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	347,	ence 347, App
Sequence Sequence Sequence Sequence Sequence	Seque	Seque	Seque	Seque	Seque	Seque	Sequence	Seque	Seque	Sedne	Seque	Sedne	Sedne	Seque	Sedne	Sequence	Sequence	Sedne	Seque	Sedne	Seque	Sedne	Sedne	Sedue	Sedne	Seque	Sedne	Seque	Sedue	Sedne	Sedne	Segue	Sedne	Sedne	Segue	Sedne	Sedne	Sedue	Sedne
US-10-184-623-347 US-10-184-635-347 US-10-184-637-347 US-10-184-646-347 US-10-184-647-347 US-10-184-652-347	us us us	US US	ds -s	us-	US-10-180-542-347 US-10-180-548-347	US-10-180-551-347	0-180-998- 0-180-999-	US-10-183-013-347 US-10-184-612-347	US-10-184-616-347	1-184-622-	US-10-184-628-347	0-184-630-	US-10-184-631-347 US-10-184-632-347	US-10-184-636-347 US-10-184-640-347	0	20	US-10-187-597-347 US-10-187-598-347	9 5	000	10-	010	٠,	US-10-187-753-347	01.0	US-10-187-884-347	US-10-188-767-347	US-10-188-770-347	US-10-188-773-347 US-10-188-781-347	US-10-194-361-347	US-10-194-423-347	US-10-195-901-347	US-10-196-756-347 US-10-173-708-347	US-10-176-479-347	US-10-176-916-347	US-10-179-507-347	9-51	US-10-179-525-347	US-10-180-540-347 US-10-180-545-347	3-00
3871 3871 9871 9871 9871 9871					871 9 871 9	871 9	871 9	871 9 871 9	871 9	871 9	871 9	871 9	871 9 871 9	871 9	871	871 9	871 9 871 9	871 9	871 9	871 9 871 9	871 9 871 9	3871 9	871 9	871 9	871	871 9 871 9	871	871 9	871 9	871 9	871 9	871 9 871 9	871 9	871 9	871 9	871 9	871 9	871 9	871 9
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बंबंबंबंद् - ८८८८	बंबंब ८८८	444	i 4i 4i	4.4	4.4	4.	4 4.	4.4	4.4	4	4.4	4	4 4	4.4	. 4.	44	44	4.4		4.4	4.4	15	44	4.4	4	4 4		4 4	4.	4.4	4.	14 7	4.	44	4.	4 4	4.	4 4	4
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Sequence Sequence Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 347, App	Seguence 347, App Seguence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App	Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	Sequence 347, App Sequence 347, App	Sequence 347, App	347,	equence 347,	Sequence 347, App Sequence 347, App	equence 347,
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9 US-10-111-817-557 Sequence US-10-111-817-557 Sequence US-10-131-8278-557 Sequence US-10-131-8188-557 Sequence US-10-131-8188-557 Sequence US-10-131-8188-557 Sequence US-10-131-8188-557 Sequence US-10-131-8188-557 Sequence	9 US-10-137-869A-357 Sequence 9 US-10-147-523-357 Sequence 9 US-10-158-785-357 Sequence	9 US-09-978-1878-495 Sequence 9 US-10-121-042-357 Sequence	10 US-09-974-300-174 Sequence 10 US-09-7742-373-10 Sequence	9 US-10-198-846-13852 Sequence	9 US-10-174-590-347 Sequence 9 US-10-176-758-347 Sequence	9 US-10-175-737-347 Sequence	9 US-10-173-706-347 Sequence 9 US-10-175-738-347 Sequence	9 US-10-175-752-347 Sequence 9 US-10-176-482-347 Sequence	9 US-10-176-757-347 Sequence	9 US-10-180-552-347 Sequence	9 US-10-180-557-347 Sequence	9 US-10-174-572-347 Sequence	9 US-10-174-579-347 Sequence 9 US-10-174-582-347 Sequence	9 US-10-174-588-347 Sequence	9 US-10-175-740-347 Sequence	9 US-10-175-743-347 Sequence 9 US-10-176-488-347 Sequence	9 US-10-176-492-347 Sequence 9 US-10-176-747-347 Sequence	9 US-10-176-750-347 Sequence	US-10-176-987-347 Sequence	9 US-10-176-991-347 Sequence 9 US-10-176-992-347 Sequence	9 US-10-176-993-347 Sequence	9 US-10-173-695-347 Sequence	9 US-10-1/3-59/-34/ Sequence 9 US-10-173-705-347 Sequence	9 US-10-174-576-347 Sequence	9 US-10-174-586-347 Sequence	9 US-10-175-747-347 Sequence	9 US-10-176-485-347 Sequence	9 US-10-176-487-347 Sequence 9 US-10-176-493-347 Sequence	9 US-10-176-756-347 Sequence	9 US-10-176-911-347 Sequence 9 US-10-176-919-347 Sequence	9 US-10-176-925-347 · Sequence	9 US-10-176-978-347 Sequence 9 US-10-179-510-347 Sequence	9 US-10-180-543-347 Sequence	9 US-10-180-544-34/ Sequence 9 US-10-180-546-347 Sequence	9 US-10-180-547-347 Sequence	9 US-10-180-549-347 Sequence 347, 9 US-10-180-555-347 Sequence 347,	9 US-10-180-559-347 Sequence 347,	9 US-10-181-000-347 Sequence 347, 9 US-10-183-010-347 Sequence 347,	9 US-10-183-012-347 Sequence 347,
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20000000000000000000000000000000000000	11-13139 13139, Ap. 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192002 192
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NESULT 1 US-09-864-77 US-09-864-77 COURENT NO PAPELICAN APPLICAN A

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APPLICANT: Harzel, David K.
APPLICANT: Chen, Membhang
TITLE OF INVENTION: HUMAN PEROME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AP000120.1
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN HELLO, SIGNAL = 0.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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PRIOR APPLICATION WORRER: US 60/207,456

PRIOR APPLICATION WORRER: US 60/207,456

PRIOR APPLICATION WORRER: US 09/632,366

PRIOR PRIOR PRIOR 2000 0-03

PRIOR PRIOR PRIOR 2000 0-04

PRIOR PRIOR PRIOR 2000 0-04

PRIOR PRIOR PRIOR 2000 0-04

PRIOR PRIOR PRIOR 2001 0-04

PRIOR PRIOR PRIOR 2001 0-04

PRIOR PRIOR TANNO DATE: 2001 0-130

PRIOR PRIOR APPLICATION WORRER: PCT/USO1/0066

PRIOR PRIOR TANNO DATE: 2001 0-130

PRIOR PRIOR TANNO DATE: 2001 0-130

PRIOR PRIOR APPLICATION WORRER: PCT/USO1/0067

PRIOR PRIOR APPLICATION WORRER: 2001 0-130

PRIOR PRIOR APPLICATION WORRER: 2000 0-130

PRIOR PRIOR APPLICATION WORRER: 2001 0-130

PRIOR PRIOR APPLICATION WORRER: US 09/744,203

PRIOR PRIOR APPLICATION WORRER: US 09/774,203

PRIOR PRIOR APPLICATION WORRER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGGATGATTGGAATGTTCTTTC 180
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FRIOR FILING DATE: 2000-09-27

RIOR APPLICATION NUMBER: PCT/USO1/00666

RIOR APPLICATION NUMBER: PCT/USO1/00667

RIOR FILING DATE: A001-01-30

RIOR APPLICATION NUMBER: PCT/USO1/00667

RIOR FILING DATE: A001-01-30

RIOR FILING DATE: A001-01-30

RIOR FILING DATE: A001-01-30

RIOR PLING DATE: A001-01-30

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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 20213, Application US/09864761

PREMAL INFORMATION STATEMENT STATEM
17482 ACTITATCCAATITCACACAGAGGAGGAGGAGGATCTTCGGAAGGATTTTATTACTTAT 17541
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APPLICANT: ATROId Danna
TITLE ATROID DANNOR: Amblodye structure of chromosome: 12 TILE REPERFORCE: 1030 TOWNERS: 1031 TILE REPERFORCE: 1030 TOWNERS: 105/10/227,195A
CURRENT PILLING DATE: 2002-11-18
NUMBER OF SRD ID NOS: SRD 
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100.0%; Pred. No. 1.8e-90;
Mismatches 0;
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; Publication No. US20030077633A1
; GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Human
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US-09-864-761-20233
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CURRANT APPLICANTON NUMBER 10/10/000,1518
NUMBER OF SEQ 1D NOS: 5
SEQ 1D NOS: 5
SEQ 1D NOS: 5
LENGTH: 732
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Publication No USSO30077633A1
GENERAL HOROMATION:
APPLICANT: Corr. David
RTILE OF INVENTION: Haplocype structure of chromosome 21
FILE NEERENCE: 1030101
CURRENT APPLICATION Haplocype structure of chromosome 21
CURRENT APPLICATION HAPLOCYPE STRUCTURE OF CHROMATION: Haplocype STRUCTURE OF THIMS DATE: 2007-11-18
NUMBER OF SEC ID NOS: SOFTWARE: PASTED FOR MINDOWS VETSION 4.0
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| LOCATION: 115, 7294, 36973, 66372, 76921, 81512, 88727
| OTHER INFORMATION: n = G or C
| US-10-227-1298-1
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Pred. No. 1.3e-90;
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Publication No. US20030013136A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 181; Conservative
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US-10-000-1518-5
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ORGANISM: Human
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Sequence 89, Application US/09772134B
| Patent No. US2002014310A1
| Patent No. US2002014310A1
| Patent No. US2002014310A1
| APPLICANT: Southern Illinois University
| APPLICANT: LightCoc, David
| APPLICANT: LightCoc, Dav
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1. OFHER INPOMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
2.09-772-1348-89
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                                                                                                    Sequence 10553 Application US/09867701
Peterat Mo. US2002012217A1
GRNEAL INFORMATION: 1230
APPLICANT: Adate.
APPLICANT: Adate.
APPLICANT: Hone, Robert
TITLE GANT: WITHER COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE REPRENCE: 130.121.497
CURRENT FILLING DATE: 2001-05-29
SOFTWARE: FELSE DE DE Windows Version 4.0
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Pred. No. 5.1;
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- Sequence 7019 Application US/09867701

- Patent No. US2002013227A1

- GBNEAL INCHMATTON:

- APPLICANT: AGJACE, Paul A.
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CORGANISM: Homo sapien
US-09-867-701-10563
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ORGANISM: soybean
                                                                     -09-867-701-10563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGG 167
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OTHER INCORMATION: REPRESSED IN BEONE WARROW, SIGNAL = 1.1

OTHER INCORMATION: EXPERSED IN BEONE WARROW, SIGNAL = 1.1

OTHER INCORMATION: EXPERSED IN MEDIA. INCERNAL = 1.3

OTHER INCORMATION: EXPERSED IN HEART, SIGNAL = 1.4

OTHER INCORMATION: EXPERSED IN HEART, SIGNAL = 1.4

OTHER INCORMATION: EXPERSED IN PLACENTA, SIGNAL = 1.4

OTHER INCORMATION: EXPERSED IN PLACENTA, SIGNAL = 1.1

OTHER INCORMATION: EXPERSED IN HEATA, SIGNAL = 1.1

OTHER INCORMATION: EXPERSED IN INFA, SIGNAL = 1.7

OTHER INCORMATION: EXPERSED IN LING, SIGNAL = 0.94

OTHER INCORMATION: EXPERSED IN LING, SIGNAL = 0.94

OTHER INCORMATION: EXPERSED IN 18744, SIGNAL = 0.94

OTHER INCORMATION: EXPERSED IN 18744, SIGNAL = 0.94

OTHER INCORMATION: RATHERSED IN LING, SIGNAL = 0.094

OTHER INCORMATION: RATHERSED IN LING, SIGNAL = 0.094

OTHER INCORMATION: RATHERSED IN LING, SIGNAL = 0.004

OTHER INCORMATION: RATHERSED IN LING, SIGNAL = 0.004

OTHER INCORMATION: NOT HIT: AP202095.1, EVALUE 0.006+00
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PRIOR FILING DATE: 2000-05-26
RRIOR APPLICATION WOMER: US 09/632,366
RRIOR APPLICATION WOMER: US 03/632,366
RRIOR APLICATION WOMER: US 06/236,359
RRIOR PILING DATE: 2000-10-04
RRIOR PLING DATE: 2000-10-27
RRIOR PILING DATE: 2000-09-27
RRIOR PILING DATE: 2001-01-30
RRIOR APLICATION WHORE: PCT/USO1/00669
RRIOR PILING DATE: 2001-01-30
RRIOR APLICATION WHORE: PCT/USO1/00669
RRIOR PLING DATE: 2001-01-30
RRIORHAN SANDER DATE: 2001-01-30
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 1925, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INFORMATION:
| APPLICANT Hyeag, IN. PROM VARIOUS COND. LIBRARIES
| TITLE OF INVERTION: PROM VARIOUS CDNA LIBRARIES
| TITLE OF INVERTION: PROM VARIOUS CDNA LIBRARIES
| CURRENT APPLICATION NUMBER: US/09/918,995
| CURRENT PELLING DATE: 2001.07.30
| PRIOR FILING DATE: 1999.01.07.30
| PRIOR FILING DATE: 1999.01.07.30
| PRIOR FILING DATE: 1999.01.07.30
| SEQ ID NOS: 38054
| SEQ ID NOS: 38054
                                                                                                                                                                                                                     Length 475
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                                                                                                                                                                                                                                                                                0; Indels
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18;
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                                                                                                                                                                                                                Query Match 9.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 18; Matches 17; Conservative 0; Mismatches
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SOFFWARE: FastSEC for Windows Version 4.0
SEC ID NO 1
LENGTH: 1397
LYPE: DNA
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US-09-918-995-1925
                                                           NAME/KEY: misc_feature
LOCATION: (1)...(475)
OTHER INFORMATION: n = A,T,C or US-09-218-995-69
                                                                                                                                                                                                                                                                                                                                                                                                       204 GAGCAAGAGCCCTCCA 220
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Homo sapiens
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US-09-778-171-1
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US-09-778-171-1/c
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Farent No. 102002013233.41
GENERAL INCORMATION: APPLICANT ADJACE AND APPLICANT ADJACE SUSAN A APPLICANT ADJACE SUSAN A APPLICANT ADJACE SUSAN L. APPLICANT ADJACE SUSAN L. APPLICANT ADJACE AND DIAGNOSIS OF OWARIAN CANCER FILE OF INVERTION: COMPOSITIONS AND DIAGNOSIS OF OWARIAN CANCER FILE REPRESENCE 2010.14.97
CORRENT ADJACE AND TOWNERS. 1050.20
SOUTHERS: PRESENCE 2010.14.97
NOMBER OF ESCUENCE 1031.2
SOUTHERS: PRESENCE OF WINDOWS VEFSION 4.0
LENGTH: 375
LENGTH: 375
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APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: HATLOCKET SUSAN
TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR THE THEREPY
TITLE OF INVERTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPRESENCE: 210121.497
FULE REPRESENCE: 210121.497
FULE STEPRESENCE: 210121.497
FULE STEPRESENCE: 210121.497
FULE OF INVERTION ANTER: 20011.05-29
SOUTHARE: PRESENCE FOR WINDOWN VERSION 4.0
SEQUENCE: 200121.407
SEQ
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TITLE OF INVENTION:

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC CHARAITES
FILE REPRENCE: 2011-76
CURRENT APPLICATION NUMBER: US/09/19, 995
CURRENT FILIKO DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR RELING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFFWARE: PELSEQ for Windows Version 3.0
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100.0%; Pred. No. 18;
tive 0; Mismatches
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9.4%; Score 17;
Best Local Similarity 100.0%; Pred. No.
Matches 17; Conservative 0; Mismatc
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US-09-310-995-69
: Sequence 69, Application US/09918995
: Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CTCCAAGCCAAAGTTGA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 CTCCAAGCCAAAGTTGA 119
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Best Local Similarity 100.C
Matches 17; Conservative
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ORGANISM: Homo sapiens
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US-09-867-701-7019
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US-09-867-701-7022
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US-09-867-701-7022
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9.4%; Score 17; DB 10; Length 465237; llarity 100.0%; Pred. No. 28; Conservative 0; Mismatches 0; Indels 0;
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Patent No. US20020121095A1
GENERAL INFORMATION
TITLE OF INVESTION. Exceptor alpha variants and
TITLE OF INVESTION. Exceptor alpha variants and
TITLE OF INVESTION. Exceptor facection thereof
CURRENT PILING DATE. 2010-08-21
CURRENT FILING DATE. 2010-08-21
REIGH APPLICATION NUMBER: 66/16026
REIGH APPLICATION NUMBER: 66/16026
REIGH APPLICATION NUMBER: 66/16026
REIGH APPLICATION NUMBER: 66/16026
REIGH APPLICATION NUMBER: 09/269414
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APPLICANT: JonedGettr, Sigridur Th.
TITLE OF INVENTION HUMAN STROKE GENE
FILE REPRENCE: 1345-200-03
CURRENT APPLICATION NUMBER: US/J0/067,514
CURRENT FILEM DATE: 2002-02-04
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FactSCO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 465237
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; Sequence 12596, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 ATTTTTATTACTTATAT 62
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Matches 17; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: human
US-09-933-267A-1
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Pred. No. 25;
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100.0%; Pred. No. 24;
tive 0; Mismatches 0; Indels
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SOFTWARE PATEMENT Ver. 2.0
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Patent No. US/200059473A1
PREMAINED THOUGHATION
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APPLICANT SHOUL NO. WHELE
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TIPLE OF INVENTION. AND SHOUL NO. BULLET
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7358, Application US/09764891
PUBLICATION NO. US20033077808A1
PUBLICATION NO. US20033077808A1
APPLICATION NO THE TITLE OF THE 
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CURRENT APLICATION NUMBER: US/09/854 883
CURRENT PLIANG DATE: 2001-05-14
PRIOR APPLICATION WHERE: US 09/629,644
PRIOR PLIING DATE: 2000-07-31
PRIOR PLIING DATE: 2000-07-31
PRIOR PLIING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 389
SEQ ID NO 24 1 NOS: 389
LENGTH: 78899
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                                                                                                                    248 CACACAGACGCTGGAAG 232
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                                                                15 CACACAGACGCTGGAAG 31
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Best Local Similarity 100.1
Matches 17, Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-764-891-7358
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-764-891-7358
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US-09-933-267A-1
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| Sequence 1502, Application US/09938842A | Sequence 1502, Application US/09938842A | Sequence 1502, Application US/09938842A | Settent No. USZ0020166378A1 | Settent No. USZ0020166378A1 | Sequence 1502, Application | Applicant Reps, Josi | Applicant Reps, Josi | Applicant Wang, Minn STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING | TITLE OF INVENTION: SAME, AND METHODS OF USE | TITLE OF INVENTION: SAME, AND METHODS OF USE | CORRENT Applicanton Numbers 155/09/938, 442A | CORRENT APPLICANTON NUMBER: 125/09/938, 442A | SHOR APPLICANTON WANGER: 125/09/938, 442A | SHOR APPLICAN
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APPLICANT: MacLet, John H.
APPLICANT: MacLet, John H.
APPLICANT: Gation, Theodore J.
APPLICANT: Gation, Theodore J.
APPLICANT: Gation, Theodore J.
APPLICANT: Gation, Theodore J.
APPLICANT: Pord, Donna M.
APPLICANT: Pord, Donna M.
APPLICANT: Pord, Donna M.
APPLICANT: Marchan, John E.
APPLICANT: MacChiegel, Robert
TITLE OF TRYENTION NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF TRYENTION NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF TRYENTION NOVEL HUMAN GENES AND GENE EXPRESSION
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8.8%; Score 16;
Best Local Similarity 100.0%; Pred. No.
Matches 16; Conservative 0; Mismatch
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                         Steinmann, Kathleen E.
Astle, Jon H.
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1502
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SEQ ID NO 1502
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ORGANISM: Homo sapiens
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APPLICANT: Tao, Neeley C.
APPLICANT: Tao, Neepling
APPLICANT: Tao, Neepling
TITLE OF INVENTION: MIGCLE ALI DATE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MIGCLE ALI DAD BEDSITION
TITLE BERRENCIE: 16511 006/37-21 (10298)
CURRENT PLILATION DATE: 2001.09-24
CURRENT PLILATION DATE: 2001.09-24
KNUMBER OF SEO ID NOS: 15112
LENGTH: 324
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APPLICANT: Tao, Wegbing
APPLICANT: Tao, Wegbing
APPLICANT: Tao, Wegbing
APPLICANT: Methiad again, Negappan
TITLE OF INVENTION: WIGHER AND FAT DEBOGITION
TITLE OF INVENTION: WIGHER AND FAT DEBOGITION
FILE REPRENCE: 37-21(1022))C
CURRENT PELLORION NUMBER: US/09/983,965
CURRENT PILING DATE: 2001-10-26
PRIOR PELLORION NUMBER: US 69/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
WIGHER OF SEQ ID NOS: 59.12-7
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8.8%; Score 16; DB 10; Length 324;
Beet Local Similarity 100.0%; Pred. No. 63;
Matches 16; Conservative 0; Mismatches 0; Indels
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8.8%; Score 16; DB 10; Length 438;
Beet Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels
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LOCATION: 1355), (425)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 20-LIB3058-009-Q1-K1-E7
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Patent No. US20020137160A1
GENERAL INFORMATION:
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Sequence 381, Application US/09879536
Patent No. US20020144298A1
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ORGANISM: Bos taurus
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ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
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LENGTH: 438
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Page 15

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Sequence 16, Application US/09851129A
Partent No. US2020215466A1
APRILONT: INTEREST DENIES
APPLICANT: APPLICANT: MATHIAS
APPLICANT: MATHIAS
TITLE OF INVENTION: VACCULAR SPECIFIC REQUIATORY ELEMENTS CONTAINED IN THE
TITLE OF INVENTION: S. P. FLANKING REGION
FILE REPREBURE: 0525040450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. 1920020053108A1

GREENT NO. 1920020053108A1

FPLICANT Rosen et al.

TITLE RIFERENCE: PAD 100.

CURRENT FILING DATE: 200.049/925,301

CURRENT APPLICATION NUMBER: US/09/925,301

REIOR PILING APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 200.049/905,301

PRIOR PILING APPLICATION NUMBER: 05/124,270

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Recently Ver. 2.0

SEQ ID NOS: 1894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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100.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.01; Pred. No. ...
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
PRIOR APPLICATION NUMBER: US/60/235,030
PRIOR PLILIDE DATE: 2000-09-28
PRIOR PLILIDE DATE: 2000-09-28
PRIOR PLILIDE DATE: 2000-09-27
PRIOR PLILIDE DATE: 2000-99-27
PRIOR PLILIDE DATE: 2000-99-27
NUMBER CF SEQ ID NGS: 2256
SEGTHARE: PRICHILD VETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 TTATATGGACAATTGG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-954-456-1838
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Petern Wo. USZOGISISOSTAL
GRAECAL INPORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: See 189290-74
TITLE OF INVENTION NUMBER: US/60/33.617
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PRIOR APPLICATION NUMBER: US/60/235,637
                                                                                                                                                                                                                              GARGALAL INFORMATION:

APPLICANT: Young, Paul

TITLE OF INVENTION: Secs

FILE OF INVENTION: Secs

CURRENT APPLICATION WARER: US/09/954,456

CURRENT APPLICATION WARER: US/05/023,617

PRIOR APPLICATION WARER: US/05/023,617

PRIOR APPLICATION WARER: US/05/023,613

PRIOR APPLICATION WARER: US/05/023,511

PRIOR APPLICATION WARER: US/05/023,511

PRIOR APPLICATION WHORE: US/05/023,618

PRIOR APPLICATION WHORE: US/05/023,619

PRIOR APPLICATION WHORE: US/06/023,619

PRIOR APPLICATION WHORE: US/06/023,619

PRIOR APPLICATION WHORE: US/06/023,619

PRIOR APPLICATION WHORE: US/06/023,619

PRIOR APPLICATION WHORE: US/06/0235,619

PRIOR PLINED APPLICATION WHORE: US/06/0235,619

PRIOR PLINED APPLICATION WHORE: US/06/0235,619

PRIOR PLINED APPLICATION WHORE: US/06/0235,619
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                                                                                                                                                                   Sequence 1174, Application US/09954456
Patent No. US20020115057A1
   458 AAGTTGATGCTGAGAA 473
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-954-456-1838
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LENGTH: 2244
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APPLICANT. Augusting, Meesa
TITLE OF INVARITON: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVARITON: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVARITON: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVARITON: MARMER: US/09/969,708
TITLE PRINCE PRINCE APPLICATION NUMBER: US/09/237,606
RECORDED FOR APPLICATION NUMBER: US/00/237,608
RECORDED FOR APPLICATION NUMBER: US/00/237,608
RECORDED FOR APPLICATION NUMBER: 2000-10-03
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Publication No. US20030100528A1
GENERAL INFORMATION:
APPLICANT: Allieri, Dario C.
ITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
CELLULAR APOPTOSIS, AND ITS MODULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 11990;
80;
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REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
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ADDRESSEE: MORGAN, LEWIS & BOCKIUS
STREET: 1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 1
Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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COUNTRY: USA
ZIP: 20016-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
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Matches 16; Conservative 0;
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US-09-969-708-569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 569
LENGTH: 11990
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Patent No. USZ0020115657A1
Patent No. USZ0020115657A1
Patent No. USZ0020115657A1
The Cancer TherePatent Normal Patent 
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100.0%; Pred. No. 76;
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CURRENT PILIDA DATE: 2001-09-18
FRIOR APPLICATION NUMBER: U8/60/248
RRIOR PILIDA DATE: 2001-09-18
FRIOR PELICATION NUMBER: U8/60/214,052
FRIOR PELICATION NUMBER: U8/60/214,052
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FRIOR PELICATION NUMBER: U8/60/214,023
FRIOR PELICATION NUMBER: U8/60/214,023
FRIOR FILING DATE: 2000-09-25
FRIOR PELICATION NUMBER: U8/60/215,617
FRIOR PELICATION NUMBER: U8/60/215,617
FRIOR PELICATION NUMBER: U8/60/215,617
FRIOR PELICATION NUMBER: U8/60/215,618
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FRIOR PELICATION NUMBER: U8/60/215,720
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CURRENT APPLICATION NUMBER: US/09/851,129A
CURRENT PLING DATE: 2001-05-09
RIOR APPLICATION NUMBER: 09/165,098
RHORP FLING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VEY: 3.1
ERROTH: 2889
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Patent No. US20020102532A1
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Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 498
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Matches 16; Conservative
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ORGANISM: Human
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Applicant: C. Frank Bennett

Applicant: Eliabeth U. Ackermann

Applicant: Eliabeth U. Ackermann

Applicant: Eliabeth U. Ackermann

Applicant: Eliabeth U. Ackermann

TITLE CONTROL STATE CONTROL

TITLE RETERANT: 18 HOUSE CONTROL

CONTROL PELICATION NUMBER: US/09/918.186A

PRICE PELICATION NUMBER: 010-02-02

PRICE FLICATION NUMBER: 010-02-02

PRICE FLICATION NUMBER: 09/20-04

PRICE PELICATION NUMBER: 09/20-04

PRICE PERICE PERI
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100.0%; Pred. No. 81;
tive 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 81;
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                                                                    PRIOR ADMINATION NUMBER: US/60/234,923
PRIOR FILING DARF: 2000-09-25
PRIOR PLING DARF: 2000-09-25
PRIOR PLING DARF: 2000-09-25
PRIOR PLING DARF: 2000-09-25
PRIOR PLING APELICATION NUMBER: US/60/25,14
PRIOR PLING DARF: 2000-09-26
PRIOR PLING DARF: 2000-09-26
PRIOR PLING DARF: 2000-09-27
           US/60/234,052
                                             FILING DATE: 2000-09-20
APPLICATION NUMBER: US/60/234,923
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Patent No. US20020137708A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 1636
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, LOCATION: (11955)...(12044)
US-09-918-186A-3
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Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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NAME/KEY: CDS
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ORGANISM: Homo sapiens
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PRENERAL INPORMATION

APPLICATI: VOUNGARATION

TITLE OF INVENTION SEE FOR EACH CANDING ANTI-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION SEE FOR EACH CANDING SEE SOOT SEE FOR EACH CANDING SEE SOOT SEE FOR EACH CANDING SEE SOOT 
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Sequence 16.5. Application US/09954456
GENERAL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Set
FILE REFERENCE: 69920-7 (Set)
FILE REPRENCE: 69920-7 (Set)
FILE REPRENCE: 10.5019-19
FRICK PAINTY FILING DATE: 2001-09-18
FRICK PAINTY FILING DATE: 2000-09-18
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81;
                                                                                                                       Match B.8%; Score 16; DB 9; Length 14796;
Local Similarity 100.0%; Pred. No. 81;
les 16; Conservative 0; Mismatches 0; Indels
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8.8%; Score 16; DB
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-138-618-35
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-954-456-1636
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                                                                                                                                  Query Match
                                                                                                                                                                                                            Matches
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Sequence 1 Application US/10185770

GENERAL INFORMATION: 052030022117A1

GENERAL INFORMATION: 052030022117A1

APPLICATOR : CECCARDI TOLI Et al.

APPLICATOR: CECCARDI TOLI Et al.

ITILE DE INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND ITILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND ITILE OF INVENTION: USES THERROF CID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND ITILE OF INVENTION: USES THERROF CID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND ITILE OF INVENTION WORDS: 03/01/05/27000 PRICE FILING DATE: 2001-07-02

NUMBER FILING DATE: 2001-07-02

NUMBER FILING DATE: 2001-07-02

NUMBER FILING DATE: AND SA 4
                                                                                                           REPLICANT: Bone, David
APPLICANT: Bone, Derek
APPLICANT: Bone, Derek
APPLICANT: Minczak, Leszek
APPLICANT: Leszek
APPLICANT: Leszek
APPLICANT: Leszek
APPLICANT: Leszek
APPLICANT: Leszek
APPLICANT: Relang-Paesac, Michael
APPLICANT: Relang-Paesac, Michael
APPLICANT: Relang-Paesac, Michael
APPLICANT: Relang-Paesac, Michael
APPLICANT: Leszek
APPLICANTON HOMBER: US/AJ/176,523
CURRENT APPLICATION NUMBER: US/AJ/176,523
CURRENT APPLICATION NUMBER: US/AJ/176,523
CURRENT APPLICATION NUMBER: US/AJ/176,524
REIOR APPLICATION NUMBER: US/AJ/176,524
REIOR APPLICATION NUMBER: US/AJ/176,526
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REIOR APPLICATION NUMBER: US/AJ/176,526
REIOR REILING NUMBER: US/AJ/176,936
REIOR REILING NUMBER: US/AJ/196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 9; Length 123192;
Pred. No. 92;
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, OTHER INFORMATION: n = A,T,C or G
US-10-185-770-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118578 GGATTTTTATTACTTA 118593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GGATTTTTATTACTTA 59
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No. US20030096264A1
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 123192
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US-10-185-770-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                          US-09-880-107-3421
Sequence 3421. Application US/09880107
Facent No. US20020142931A1
FAPLICANT: WOCKLEY, JOSEPH G.
APPLICANT: WOCKLEY, JOSEPH G.
APPLICANT: OCKLEY, JOSEPH G.
APPLICANT: Gene Logic, Inc.
TITLE REPERENCE: 4492-502-40
CURRENT PRILIGANTON NUMBER: US/09/880,107
CURRENT PRILIGANTON NUMBER: US 60/211,379
PRIOR PRILICANTON NUMBER: US 60/211,379
PRIOR PRILICANTON NUMBER: US 60/211,379
PRIOR PRILICANTON NUMBER: US 60/211,379
FRIOR PRILICANTON UMBER: US 60/211,379
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FRIOR PRILICANTON UMBER: US 60/231,054
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US-09-880-107-3421
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Best Local Similarity 100.04; Pred. No. 85;
Matchea 16; Conservative 0; Mamachies 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14796;
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SOFTWARE: Patentin Ver. 2.0
SEQ 1D 0759
LEWOTH: 31314
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Parent No. US2002001714001
Parent No. US2002001714001
APPLICANTINES
APPLICANTINES
TITLE OF INVENTION: No. 1st Acids, Proteins, and Antibodies
TILE REPERENCE: POCOS
CURRENT APPLICATION NUMBER: US/09/764,877
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Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0.
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                                                                                                                            10809 ATTTTTATTACTTATA 10824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 ATTTTTATTACTTATA 61
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                                             46 ATTTTTATTACTTATA 61
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ORGANISM: Homo sapiens
US-09-764-877-3875
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US-09-764-877-3875/c
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US-10-175-523-71
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Sequence 2335, Application US/0964761
Parent No. US200200407531
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Harsel, David K.
APPLICANT: HOWN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL POR TITLE OF INVERTIONS: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                               Gaps
                                                                                                             0
                                                                       8.8%; Score 16; DB 10; Length 684973; 100.0%; Pred. No. 1e+02; 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: MAP TO ACO18528.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
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                                                                                                                                                41 GAAGGATTTTTATTAC 56
                                                                       Query Match
Best Local Similarity 100.4
Matches 16; Conservative
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ORGANISM: Homo sapiens
  ; STRANDEDNESS:
; TOPOLOGY: 111
US-09-263-959-1
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APPLICANT: Neod, Leroy E.
APPLICANT: Neod, Lee
THIRD COMPOSITIONS AND METHODS WHICH UTI
WHOREN OF INVENTION: DIAGNOSIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
WHOREN OF SECURIORS: 1.27199
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                               APPLICANT: MATANARE, HIDEAT
APPLICANT: HATTORIA MASAHER
APPLICANT: HATTORI MASAHER
APPLICANT: SANAKI, VOSHIYUKI
APPLICANT: SANAKI, VOSHIYUKI
APPLICANTO: MASHORE DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE SPERBANCE: 081156/0159
CURRENT PILLIANTO MARBER: 12007-02-23
PRIOR FILING DATE: 2000-04-07
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haa 0; Indels
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COMPUTER READALE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
RPLICATION NUMBER: 0409/263,959
FLINGO ANTE: 05-MAR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                        Sequence 1, Application US/09790988
Patent No. US20020127687A1
GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
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NAME: POMBAREES, DAVID 0.
REGISTRATION UNDRER: 33,963
REFERENCE/COCKET WINERE: 9200.
TELECOMMUNICATION INFORMATION:
TELETRAM: (206) 622-4900
TELETRAM: (206) 622-4911
INFORMATION FOR SEQ 16 NO. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324454 TGGTGATGATTGGAAT 324439
98266 TACTTATATGACAAT 98281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 TGGTGATGATTGGAAT 170
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                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 640681
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Matches 16; Conservative
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ADDRESSEE: Seed and
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CITY: Seattle
STATE: Washington
COUNTRY: US
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ORGANISM: Buchnera sp.
US-09-790-988-1
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                                                                                           JS-09-790-988-1/c
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Sequence 464, Application US/0991936
| Publication No. US20010073827A1
| CHARLE APPLICANT | WISHORS, Nancy | TITLE OF INVENTION: PICA HEAD, NREWE CORD, HINDGUT AND WALPIGHIAN TUBULE | TITLE OF INVENTION: PICA HEAD, NREWE CORD, HINDGUT AND USES THEREOF | TITLE OF INVENTION: PICA HEAD, NUMBER: US/09/991,936 | CURRENT FILLOW DATE: 2001-11-21 | CHARLE APPLICATION WHORER: US/09/991,936 | CURRENT FILLOW | DATE: 2001-11-21 | CHARLE APPLICATION WHORER: US/09/991,936 | CHARLE APPLICATION WHORE DE SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHO SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1959 | CHARLE APPLICATION WHORE OF SED ID NOS: 1950 | CHARLE APPLICATION WHORE OF SED ID NOS: 1950 | CHARLE APPLICATION WHORE OF SED ID NOS
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                                                                                 APPLICANT Davis, 'eith R.
APPLICANT Davis, 'eith R.
APPLICANT ALIAN Keith
APPLICANT HOffman, Weith
APPLICANT WINDON, PARTING BERTHAND, PARTING BERTHAND, PARTING BERTHAND, PARTING BERTHAND BERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 15; DB 9; Le
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 583
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 20062, Application US/09864761 ; Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Arabidopsis thaliana
US-09-770-696-583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TTGATGCTGAGAACT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AAGCCAAAGTTGATG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 TIGATGCTGAGAACT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-864-761-20062
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APPLICAMT: Sambrowicz, Brian
TITLE OF INVENTION: NO. U625020110809Alel Human Polynucleotides and the
TITLE REPREBNUE: LOB-0018-048
CURRENT PELLING NO. 10018-04-28
FRIOR APPLICATION NUMBER: US-001-04-28
FRIOR APPLICATION NUMBER: US-001-04-28
SROFWARE: FastSEQ for Mindows Version 4.0
SSO ID NOS: 1008
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CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
COTHER INFORMATION: EXPRESSED IN FATAL LIVER, SIGNAL = 1.4
COTHER INFORMATION: EXPRESSED IN BEATAL SIGNAL = 1.8
COTHER INFORMATION: EXPRESSED IN BEATAL SIGNAL = 1.3
COTHER INFORMATION: EXPRESSED IN HARTY, SIGNAL = 1.4
COTHER INFORMATION: EXPRESSED IN HARTY SIGNAL = 1.4
COTHER INFORMATION: EST_MOMAN HIT: LA9349.1, EVALUE 1.60e-01
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8.3%; Score 15; DB 10; L

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 0;
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8.3%; Score 15; DB 10; L

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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Patent No. US20010044940a1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Olang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 157, Application US/09560863
Patent No. US20020110809A1
GENERAL INFORMATION:
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US-09-560-863-157
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 GCTGAGCAAGAGGCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB GATTTTATTACTTA 102
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LOCATION: (1)...(133)
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ORGANISM: homo sapiens
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US-09-770-696-583/c
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APPLICANT:
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APPLICANT:
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Sequence 11763, Application US/09878574
| Peretr No. US20020110548A1
| Peretr No. US20020110548A1
| PRETRY US US20020110548A1
| APPLICANT: LA ROSE, THOMSE J.
| APPLICANT: Thompson, Mitchel D.
| ITLIE OF INVENTION: Plants D.
| ITLIE OF INVENTION: Plants US/09/878,574
| CURRENT FILE MESENCE: 39-115401)B
| CURRENT FILE MESENCE: 39-105401)B
| PRIOR FILING DATE: 1999-06-14
| WINMER: OF SEQ ID NOS: 15775
| WINMER: OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Harzel, David R.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 271;
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100.0%; Pred. No. 2.2e+02;
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Best Local Similarity 100.0%; Pred. No. 2.2
Pest Local Similarity 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701064862H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19038, Application US/09864761 Patent No. US20020048763A1
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                                        RESULT 44
US-09-878-574-11763
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US-09-864-761-19038
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THE INCORMATION EXPERSED IN PLACENTA, SIGNAL = 0.9

ER INCORMATION EXPERSED IN PR444, SIGNAL = 0.94

ER INCORMATION EXPERSED IN PR744, SIGNAL = 0.19

ER INCORMATION EXPERSED IN PRTA. LIVER, SIGNAL = 1.1

ER INCORMATION EXPERSED IN MING, SIGNAL = 3.1

ER INCORMATION EXPERSED IN MELL, SIGNAL = 3.1

ER INCORMATION EXPERSED IN MELL, SIGNAL = 1.1

ER INCORMATION EXPERSED IN MELL, SIGNAL = 1.1

ER INCORMATION EXPERSED IN HEART, SIGNAL = 1.3

EXPERIENCE IN HEART SIGNAL EXPERSED IN HEART SIGNAL S
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conservat
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION
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APPLICATION NUMBER: PCT/USO1/00663
PLILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30

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PRATICE:

OTHER INCOMMATION BENESSED IN PLACENTA, SIGNAL = 4.5

OTHER INCOMMATION BENESSED IN PLACENTA, SIGNAL = 3.4

OTHER INCOMMATION BENESSED IN PLACENTA, SIGNAL = 3.4

OTHER INCOMMATION BENESSED IN WELLA, SIGNAL = 3.4

OTHER INCOMMATION BENESSED IN WEART, SIGNAL = 4.3

OTHER INCOMMATION BENESSED IN WEART, SIGNAL = 4.3

OTHER INCOMMATION BENESSED IN BURG, SIGNAL = 4.3

OTHER INCOMMATION BENESSED IN MAINT, SIGNAL = 4.5

OTHER INCOMMATION BENESSED IN MAINT INFO. SIGNAL = 4.5

OTHER INCOMMATION BENESSED IN STALL INFO. SIGNAL = 6.6

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AX406939 732 bp Sequence 1 from Patent W00222875. AX406939 AX406939.1 GI:21439814

RESULT 1
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human. Homo sapiens

Matches   181, Conservative   0, Mismatches   0, Indels   0, Gaps   0, Gaps   0, Indels   0, Indels   0, Gaps   0, Indels   0, Indel	RESULT 4 AF302095 LOCUS AF302095 AF302095 AF302095 AF302095 AF302095 AF302095 AF302095 AF302095 ACCESSION AF302095 ACCESSION AF302095.1 GI:10121887	N N N N N	TITLE Direct Submission JOURNAL Submitted (10.5E2-2000) Medical and Molecular Genetics Center, JOURNAL Submitted (10.5E2-2000) Medical and Molecular Genetics Center, Institut Recerca Oncologica, Avia. de Castelldefels Km 2,7, I. Hospitaler de Libbregar, Barcelona 08907, Spain FEATURES Location/Qualifiers 1. 809   Castellandar   Castellandar   Castellandar     Castellandar   Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Castellandar   Castellandar     Caste	gene   1.809   49   18.805   141.512   20   20   20   20   20   20   20   2	tch alsimilarity 100.0%; Score 181; DB 9; Le 181; Conservative 0, Mismatches 0, 1  1 ACTIVATCHATTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
INFEVINITY MANAGEMENT AND THE STATEMENT AND THE	200 GCTGGGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGGAATGTTCTCTTTC 181 A 181 260 A 260		REFERENCE 1 (bases 1 to 732) AUTHORS Timochty, K.W., Keating, M.T. and Goldstein, S.A., Lehmann, M.H., TITLE MRPI forms IKr potsastium channels with HERG and is associated with Carlide arthythmed arthythmed arthythmed arthythmed arthythmed arthythmed passays FURNED 1031939 REPERENCE 2 (bases 1 to 732) AUTHORS Abbott, G.W., Sesti, F., Buck, M.E. and Goldstein, S.A.N.	JUTUE Direct Submission JOURNAL Submitted (105-1019.1998) Section of Developmental Biology and JOURNAL Submitted (105-1019.1998) Section of Developmental Biology and Biophysics, Department of Pediarrics and Boyer Center for Molecular Medicine, Yale University School of Medicine, 295 Congress Avenue, New Haven, CT 06536, USA FEATURES JOINTER LOCATION/Qualifiers SOURCE JOINTER HOMO Sapiens JOINTER HOMO Sapiens JOINTER HOMO Sapiens JOINTER HOMO SAPIENT JOINTER HOMO SAPI	CDS 74. 445.75  Total Subunit; MiRP1"  (codon grartal mennel subunit; MiRP1"  (produce="mirr-related petide 1"  (produce="mirr-related 1"  (produce="mirr-related 1")  (produc

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKRN), Genomic Sciences Center (GSC); Kiteasto Univ., 1-15-1 Kiteasto, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, Tel:81-42-778-9923; Fax:81-42-778-9923;
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Homo sapiens genomic DNA, chromouome 21q22.1, D215226-AML region,
121 GCTGAGAACTTCTACTATGTCATCCTGTACTCATGGTGATGATTGTGGATGTTCTCTTTC 180
267 GCTGAGAACTTCTACTATGATCCTGTACTGTGTATGGATGATTGTATTCTTT 2326
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1 (Base Dec. 21400) Primates Catenthin; Heminidae; Homo.

Het british I beli K. Toyoda, A. Taylor I. D., Hong-Seog, P., Pulyami, A. Nada Pammil DNA of 21422.1

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(Bases I co. 2460) Toyoda, A. Taylor, T. D., Hong-Seog, P., Pulyami, A. Yada, T. Tocoki, Y. and Sakai, Y. Hong-Seog, P., Ditect Submission
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ER Hattori, M. Ishii, K. Toyoda, A., Shiba, T. and Sakaki, Y.

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Phone: 401-3-549-5622, Fax. 481-3-5461, Sakaki, Ph.D.

Phone: 401-3-549-5622, Fax. 481-3-5449-5445, Sakakishoci ins.-trokyo.ac.jp

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and valationahip to other sequences please visit our sequence
archive Web site (http://www.alis.tokyo.ist.go.jpf.c.
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AP000052 100000 bp DNA linear PRI 20-NOV-1999
Homo sapiens genomic DNA, chromosome 21q22.1, segment 23/28,
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100.0%; Pred. No. 4.5e-93;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    Homo sapiens DNA, clone:245Pi7-f4A4f_2.
Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
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                                                                                                                                                                                               AP000052.1 GI:3132362
                                                                                                         complete sequence.
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ACCESSION

RESULT

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Homo sapiena (human)
Ebkaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia;
Ebtheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89526 ACTTTATCCAATTTCACACAGACGCTGGAAGACGTCTTCCGAAGGATTTTTATTACTTAT 89585
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/standard name="D21S1689"
14354 .44157
/note="APMa086yf9;Genethon Marker;The location is between
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                                                                                                                                                                                                                                                                                                     Submitted (15-APP-1999) to the EMBJ/GenBank/DDBJ databases with Harakawa, Japan Science and Technology corporation (1671), Advanced Databases Department; 5-3, Yonbandon, Chiyoda ku, Tokyo 102-0081, Japan (8-mail-mika@tokyo 181-90), URL:http://www-alls.tokyo.jst.go.jp/, Tal.181-15-214-4891, Fax:81-3-5214-4871)
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//moce="8359aL-F/83F9aL-R,The location is between each
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori M., Ishii K., Toyoda A., Shiba T., Sakaki Y.;
Themo saplens 817,199bp genomic DNA of 21g22.1 GART and AML region";
Unpublished.
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5-3, Yonbandro, Chiyoda-Ku, Tokyo 102-0081 Japan
For further information about this sequence, including its
location and relationship to other sequences, please visit our
sequence archive Web site (http://www.alis.tokyo.jst.go.jp/HGS/)
or send email to webmaster@www.alis.tokyo.jst.go.jp/HGS/)
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Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
The sequence is submitted by Human Genome Sequencing in ALIS
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                                                                                                                                                                                                                                               Hirakawa M., Yamaguchi H., Imai K., Shimada J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phone: +81-3-5449-5622, Fax : +81-3-5449-5445,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/sequenced_mol="DNA"
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Distect Solumisation Tocoki, Y. and Sakaki, Y.
Submitted (10 AMR-1999) Mesahira Hattori, The Institute of Physical and Chemical Research (RIKRN), Genomic Sciences Center (SSC).
Ticsacto Univ. 1. 15-1 Kitsacto, Sagaminara, Kanagawa 228-8855, Japan (E. mail. Hattoriegoc.riken.go.jp.
Pax:81-47-778-9924)
Pax:81-47-778-9924)
                                                                                                                 Makaryoca; Metaaco; Chordeta; Craniata; Vertebrata; Buteleostomi; Mammalis; Butheria; Princia; Entheria; Princia; Butheria; Princia; Princ
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100.0%; Score 181; DB 9;
Best Local Similarity 100.0%; Pred: No. 4.5e-93;
Marchee 181; Conservative 0, Mismatches 0;
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26-SEF-1999 (Rel. 61, Last updated, Version 3)
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/db_xref="taxon:9606"
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and * Max-Planck Institute for Molecular Genetics, * Theorems 23 D 14166 Boot 10 Octuber		/chromosome="2" /chromosome="2" /2940 /cyganism="Homosapiens" /db_xref="taxon:9606"	/ Chromogene="1." /map="2.422.1" /clone="1.18181", 2. partial" /clone="1.187181", 2. partial" /clone="1.187181", 2. partial" /note="Accession No. AP000467" 29142. 29150 /db xefe="taxon:9606" /db xefe="taxon:9606" /map="2422.1"	/ Cione 10.534-Firsty / Cione 10.5 - Cione	//mapw 4/422.1 /clone=n58185 /clone=11.b="CMF21 pl library" /note="Accession No. AP000116" 121210218631 /organism="Homo sapiens" /db.xref="ta.xon:9606" /chromoome="21" /map="21422.1"	/ clone= 12845p17 / clone= 11b="RPI PAC library" / note="Accession No. AP000317" 218558. 250079 / organism="Homo sapiens" / db_xref="taxon:9606" / fbp="210221" / none="Accession"	/Cione_lib_"CMP21 P1 library" /note="Accession No. AP000318" 28735. 28596 M. AP000318" /organism="Homo sapiens" /db.xref="caxon:666" /db.xref="caxon:666" /db.xref="caxon:666" /db.googne="21" /doom="219094A.D." /clone_lib="CMP21 P1 library"	/note=%Accession No. AP000319" 28573231033 /organism=Hono Gapiens" /db xref="texon:9606" /thromosome="11" /map="21422.1" /clone="202126" /clone=1202129	/ note="Accession No. AP000320" 31005035619 / cysaniam="Homo appiens" / db xrefe".cxon:9606" / chicomosome="11" / map="21g2.1" / clone="pog2F5"
is + +	FEATURES SOURCE	source	Bource	source	Bource	Bource	Bource	BOUTCE	source
89706 A 89706	AP001719 340000 bp DNA linear PRI 10-MAY-2000 H Homo sapiess genomic DNA, chromonome 21q, section 63/105. AP001719 AL163264 BA000005 AP001719. GG:776 BA000005		l (altes) Hattori M., Pujiyama A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Tyodda, A., Ishili K., Totchi, Y., Chol, D. K., Soeda, E., Ohki, M., Takagi T., Sakaki, Y., Tuudien, S., Blochschmidt, K., Polley, A., Merzel, U., Delabar, J., Kumpf, K., Lehmann, K., Parterson, D., Realchwald, K., Kump, A., Schillabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shillabya, K., Kawasaki, K., Agakwara, S., Shintani, A., Sasaki, K., Magamine, K., Mituyama, S., Horniacher, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A.,		2 (nobses 1 to 44000) Park: H. S. Tryoda, A. Taylor, T. D., Watanabe, H., Yada, T., Park: H. S., Tryoda, A. Ishi, K., Teocki, Y., Choi, D. K., Soeda, E., Ohti, M., Takagi, T., Sakaki, Y. Taudien, S., Blechschmidt, K., Polley, A., Wenzel, U., Delabar, J., Kumpf, K., Lehmann, R., Parterson, D., K. Raki, C., K. K., C., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenhal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Askawa, S., Shitteni, A., Sasaki, T., Wagamne, K., Mitsuyama, S., Antonarkis, S. E., Minchima, S., fillinizu, N., Nordsiek, G.,		Various Annual Control of Marketine Dept. of Wolecular Biology • Meat Division of Marketine Dept. of Wolecular Biology • Genome Analysis • Wax-Planck Institute for Wolecular Genetics (denome Analysis • Wax-Planck Institute for Wolecular Centics (Deforted See Deltow) on May 30, 2000 this sequence version replaced 91:771331.  On May 30, 2000 this sequence version replaced 91:771331.  First Stronger 21: Apply 30:45 and ageneting consortium consisting of Segmanhara 228-8555, Japan, 20:45 and 25:45 and 25:	and  and  institute of Molecular Biotechnology, Genome Analysis, • Beutenbergatersase 11, D-0745 Jona, Germany, • e.mail: gedj-submicgenome.imb-jena.de • URL: http://genome.imb-jena.de/ and • ted University School of Medicine, Molecular Biology, • Tokyo	• e.mail. nshind:zudehb-med.kaio.uc.jp and cuRt. http://www.dmb.med.kaio.ac.jp/ and cuBr. Dept. of Genome.Analysis. Nacoheroder weg 1. D-38124 Braunschweig, Germany, • e.mail: info.genome@pfc.de uWL: http://genome.gbf.de/
B dd	RESULT 9 APD01719 LOCUS DEFINITION ACCESSION VERSION	SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE	REFERENCE AUTHORS	TITEE	СОММЕНТ		•

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NFYVILIALWHIGHESIIVALNOSTYKSKAREHSNOPHRQYIVDMGEKTKSQILN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapians"
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74. 445
/noce="mink-calated peptide 1, Ala substitued for Thr at
aganno acid 8"
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Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Polymophisms associated with cardiac arrythmia
Patent: NO 0222875.A 9 21-MAR-2002;
YALE UNIVERSITY (US)
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Pred. No. 8.4e-84;
                                                                                                                                                                       DNA
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100.0%; Pred. No. e.
-- 0; Mismatches
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Sequence 7 from Patent WO0222875.
AX406945.
AX406945.1 GI:21439820
                                                                                                                                                                732 bp
Sequence 9 from Patent W00222875.
AX406947
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152 c
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3288 3381
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4211. 5231
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/note="(CGGG)n"
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/note="Not1 site"
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                                                                                                                                                                                       'note="AluSp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR"
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AF071003 468 bp mRNA linear ROD 29-APR-1999 Rattus norvegicus minK-related peptide 1 mRNA, complete cds.
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Cavia porcellus minK-related peptide 1 mRNA, complete cds.
                                                                                                                 80 ACTITATCCAATITCACACACACGCTGGAAGACGTCTTCCCAAGGATTTTTATTACTTAT 139
                                                                                                                                                       61 ATGGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGCCAAAGTTGAT 120
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Jianga H. at Tanga M. Liu, J. and Teeng, G.-N.
Ditect Submission
Submitted (1.2 Aug. 2001) Physiology, Virginia Commonwealth
Dinyertity, JiOI Bast Marshall Street, Richmond, VA 2328t, USA
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                    1 ACTITIATCCAATITCACACACACGCTGGAAGACGTCTTCCGAAGGAITTTTATTACTTAT
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              Score 154; DB 6; Length 732
Pred. No. 1.8e-77;
                                                  0; Indels
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                                                                                                                                                                                                                           121 GCTGAGAACTTCTACTATGTCATCCTGTACCTCA 154
                                                                                                                                                                                                                                                200 GCTGAGAACTTCTACTATGTCATCCTGTACCTCA 233
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                          100.0%; Pred. No.
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                85.1%;
                Query Match
Best Local Similarity 100.0
Matches 154; Conservative
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Rattus norvegicus
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                                                                                 /organism="Homo sapiens"
/dp.xef="taxon:9606"
/dp.445
/note="minK-related peptide 1, Thr substituted for Ile at
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Polymorphisms associated with cardiac arrythmia
Patent: WO 0222875-A 7 21-MAR-2002;
YALE UNIVERSITY (US)
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Patent: WO 0222875-A S 21-MAR-2002;
YALE UNIVERSITY (US)
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Pred. No. 1.2e-82;
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
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/tazāns laton="Wattamitotledarkki!fotledarkki]
NFYYLIKMMIGHSETVVALIVSTVKSKRREHSGHPYHOTIVEDMĢEKYKSQILH
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/Clone Ilb=WIH MCC 94"
/lab host="DH108"
/note="Vector: pCMV-SPORT6"
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/product="RIKEN cDNA 2200002116 gene"
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/clone="MGC:31447 IMAGE:4481325"
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100.0%; Pred. No. 0.0012;
tive 0; Mismatches 0;
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/db_xref="G1:18490551".
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Abbott, G. W. Searlif., Buck, M.E. and Goldstein, S.A.N.

Abbott, G. W. Searlife., Buck, M.E. and Goldstein, S.A.N.

Direct Submission

Biophysica (16-70W-1989) Section of Developmental Biology and Biophysica (16-70W-1989) Section of Bevalopmental Biophysics Department of Pediatrics and Boyer Center for Molecular Medicine, Yale University School of Medicine, 295 Congress Avenue, New Haven, CT 06536, USA

Location/Qualifiers
Abbott, G.W., Seati, F., Splawski, I., Buck, M.E., Lehmann, M.H., Timochy, K.W., Wearling, W.T. and Golderein, G.M. is associated with MRP1 forms IXr poteasium channels with HRRG and is associated with
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NFYYVILYLMVMIGMFAFIVVAILVSTVKSKRREHSQDPYHQYIVEDWQQKYRSQILH
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Musidae; Mus.
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Tissue Proutement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
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Diecet Submission
Submitted (11-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Basa, Mouston TX 77030, USA
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Direct Submission
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Submited (18-001-2002) Human Genome Sequencing Center, Department
Submited (18-001-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20162905.
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Center code: BCM (www. Mago. Com.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FEB-2002) Anatomy and Physiology, College of Veterinary Medicine, Kansas State University, 228 Coles Hall, 1600 Denison Ave. Manhattan, KS 66506-5802, USA Location/Qualifiers
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Mamalla; Eutheria, Cetartiodactyla; Suina; Suidae; Sus.
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Granulosa cells express multiple KCNQ and KCNE channel subunits
(Abstract 122)
Biophys. J. 32, 252a (2002)
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2. Undessel to 225)
Li, Y., Wymore, T., Mitchell, K.E., Wymore, R.S. and Freeman, L.C.
Direct Submission
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/codon_teat=">produce_teat="produce_teat="produce="k-fpacemaker channel beta subunit mirpl"
/produce="k-fpacemaker channel beta subunit mirpl"
/produce="k-klass271"
/produce="klass11194710"
/translation="ARRPTVILYIAWMIGMESFIIVALLVSTVKSKRREHSNDPYHQ
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Whome, R. Y., Holmes, B. A., Wymore, R. S., Yu, H., Wu, J., Potapova, I.,
Zuckern, J. T., Holmes, B. A., Wang, H., Shi, W., Robinson, R., El-Maghrabi, R.
Bernjami, W., Dixon, J. E., McKinnon, D. and Cohen, I. S.
Dixect Submission
Submitted (15-DEZ-2000) Biology, The University of Tulsa, 600 S.
College Av., Tulsa, OK 74104-3189, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ocycrolague cuniculis Bikaryota Aktaza (Craniata, Vertebrata, Buteleostomi; Bikaryota, Metazaa, Chordata, Craniata, Deportdae; Orycrolagus.
Mammalas, Butheria, Lagomorpha, Leportdae; Orycrolagus.
1 (Bases 1 to 215)
Yu, H., U., Potepova, I., Wymore, R. T., Holmes, B., Zuckerman, J., Befinain, W., Dixon, J., Meximon, D., Cohen, I. S. and Wymore, R. Befinain, W., Dixon, J., Meximon, D., Cohen, I. S. and Wymore, R. S. Wilk refated peptide 1. A beta subunit for the HCN ion channel subunit family enhances expression and speeds activation 2121148 B (12), E84-E87 (2001)
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Dast Local Similarity 100.0%; Pred. No. 0.0011;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Makethes Z6; Conservative 0; Mismatches 0; Indels 0;
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2 144709: contig of 5008 bp in length.
Location/Qualifiers
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/db_xref="taxon:9986"
                                    1. 144709
/organism="Rattus norvegicus"
/db_xref="Laxon:10116"
/clone="CH230-409A1"
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58 c 51 g 46 t
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23; Conservative 0; Mismatches
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1 (Dasses 1 to 2824), Adio-Oduola B., Ali-Osman, F.R., Allan, C., Adio-Datola B., Ali-Osman, F.R., Allan, C., Adio-Datola B., Ali-Osman, F.R., Allan, C., Alsberard, J., Banacatunger, C., Arely B., Banacatunger, R., Blankenburg, K., Bonnin, D., Bouck, J., Burker, C., Blankenburg, K., Bonnin, D., Bouck, J., Burkett, C., Blankenburg, K., Bonnin, D., Bundy, C., Burkett, C., Blankenburg, K., Branker, C., Chavez, D., Chavez, C., Colly, Doster, P., Frant, P., Dolanker, C., Edgal, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Harris, D., Charling, B., Charling, D., Larris, C., Harris, R., Harri, H., Harrison, B., Klarris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, D., Karlis, D., Korrah, J., Kovar, J., Mansson, E., Mansson, E., Mansson, E., Mansson, E., Land, J., Li, Z., Lidharge, D., Lidhar, C., Liu, J., Liux, L., Loux, D., Land, D., Manting, E., Manting, E., Mattinda, P., Martinda, M., Man, Morris, S., Charling, D., Manting, E., Minchell, T., Mohabbar, K., Mogyen, A., Matting, M., Man, C., Michar, D., Newtoon, J., N
                                                                                                                                               HTG 13-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetice, Baylor College of Medicine, One
Baylor Plaza, Houeton, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                    ## Batus norvegicus clone CH230-159K5, *** SEQUENCING IN PROGRESS P**, 50 unordered pieces.
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HTG; HTGS_PHASE1.
20 ATGATTGGAATGTTCTCTTT
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Direct Submission
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                                                                                                   RESULT 22
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   channel accessory protein; MiRP1; KCNE2"
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Patent: WO 0222875-A 13 21-MAR-2002;
VALE UNVERSITY (US)
Location/Qualifiers
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Polymorphisms associated with cardiac arrythmia
Patent: WO 0222875-A 12 21-MAR-2002;
YALE UNIVERSITY (US)
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/db_xref="taxon:32630"
/note="PCR amplification primer"
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/db_xref="taxon:32630"
/note="PCR amplification primer"
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Matches 21; Conservative
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RESULT 23
ACIOSES/C
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ACIOSES
DEFINITION Rattus norvegicus clone CH230-116N1, *** SEQUENCING IN PROGRESS
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      gap of unknown length contrig of 1153 bp in length gap of unknown length length contrig of 1291 bp in length gap of unknown length gap of unknown length is contrig of 1748 bp in length gap of unknown length
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70584; app of unknown length
73320: contig of 2736 bp in length
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/db.xref="taxon:10116"
/clone="G1230-159K5"
19368 C 18006 g 19214 t
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contig of 1242 by
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of 1209 b
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gap of unknown
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contig of 1030
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gap of unknown
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                                                                                                                                                                                                                                                                                                                                                           NOTE: Setimated insert size may differ from esquence langth (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence it currently consists of So contiges. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary, Gaps between the conflige are represented as min of N. Nut the exact sizes of the gaps are unknown. This record will be updated with the fillished are unknown. This record will be updated with the fillished are quence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                       Chemistry: Dye-terminator Big Dye, 100% of reads Assembly program: Phrapy version 0: 990329 consensus quality: 1922 bases at leart 040 consensus quality; 13922 bases at leart 040 consensus quality; 13924 bases at leart 030 consensus quality; 20254 bases at leart 020
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                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Center: Baylor College of Medicine
Center code: BCM
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gap of unknown l
contig of 1230 by
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contig of 1033 b
gap of unknown 1
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gap of unknown 1
contig of 1090 b
gap of unknown 1
                                                                                      Contact: hggc-help@bcm.tmc.edu
Project Information
Center project name: GJPX
Center clone name: GH30-159Ks
Center clone name: CH30-159Ks
Sequencing vector: plannid;
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gap of unknown l
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NOTE Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 6 contigs. The true order of the pisces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector; plasmid; Sequencing vector; plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 110567 bases at least 040 Consensus quality: 111963 bases at least 030 Consensus quality: 111803 bases at least 020 Consensus quality: 11803 bases at least 020
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Direct Submission

Direct Submission

Submitted (31.78A-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

(bases 1 to 169873)
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Submitted (11-411-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Flaza Houton, TX 77030, USA
On 11. 11. 2002 this sequence version replaced gi:18846311.
                           Center: Baylor College of Medicine
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Bathimoco, K. Osada, M., Hida, M., Kusuda, J. and Sugano, S.

Bathimoco, Robmissol Direct Submissol (25-OGT-2000) Katsuyuki Hashimoco, National Institute of Submitted (25-OGT-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-6640, Japan (6-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Takial-3-2285-1181)

Tab hose: TOP10
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Best Local
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PLN 27-DEC-2000

chromosome 5, TAC clone: K6M13

Arabidopsis thaliana genomic DNA, AB023033 BA000015 AB023033.1 GI:4220632

RESULT 25 AB023033/c LOCUS

DEFINITION

PRI 27-OCT-2000

LOCUS DEFINITION

RESULT 24 AB050510 ACCESSION VERSION KEYWORDS SOURCE

g ઠ

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

linear

A-abidopsis thaliana (strain:Columbia) DNA, clone\_lib:Mitsui TAC clone:K&M13.
Arabidopsis thaliana
Marayora, Vidiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicoryladons; orce eudicors

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complement (10191).
Product "U1 anRNA" : 10153)
Froduct "U1 anRNA" : 7"
Fortience Total K6M13 : 7"
Fortience Total S4881, 1018
Fortience Total
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FMGENLGOYKVVPRALAGGRDLGATPDIRCLEVATGLEAKGGTGBALLADFEVSE 
GTYSBACIEDTDSGVCLHJGANVLEYSGEBASALLGNNLENAKASLEVIVADLQF-XD 
OVTVTQVTIAKVYNBDVHGNRVKQTPTALANDS 
join(GodS. 126612,26693. 12616,2755). 126112) 
/noce=concalne similatity to WRKY-type DNA-binding
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QFASSNSSSFSFDTTSPELDSSSEVVTTTSPNGTSVSSS
BLAANDNSGSEVTTVADGESDQOOPGYTYDLAAKKKKKKAKARERESERVTTYSPNGTSSS
BLAANDNSGSEVTTVADGESDQOOPGYTYDLAAKKKKKKKAKARERESERPETTYSD IN
BLAANDNSGSEVTTVADGESOOPGYTYTVGCGVKKKVBRSSDGSDS WYTTVEGGHT
HPFPRTFRGHIGHLTSPLDHGATTASSSFSF ROPELADILISHOPSVRWYNNSLSAN
HRASSDGTFVNFQPSSSFPGFTDMGAKTTASSSFSTSTSKHGLLQDILDSOOIRSGTFVN
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GGCTESVSKEBHEDEBLAFTELMEBDQQL
GGCTESVSKTEBHUVBKYGTKVETPCOGSVBKDESISKOWKEBHETELMEBDQQL
GGCTESSEBEBDWYNEIDVFRPSIDANTOLYULQYPLRESWRPYEMDBCGEVT
NYRSTSQVEIDLSMOVNSKYDSWFGLAWFRQTLXTWKQPPTLDXPVGVLSGNKLHL
NVHANAQLRESWGSLESSDKXKQDESTESSVGTSKKQMKQVQASTDQKPINBETWY
NPHENAQLRESWGSLESSDKXKQDESTESSVGTSKKQMKQVQASTDQKPINBETWY
SEKYHGLQSEYCSSYLANGWBANGNSSIDPNGSFGTIKRU
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LIKLIGOPERAALDYSLEGONTY KYSSPYATOROKRULAERITSPAKERHYLDOW
KREPTDYSTISSYBETYKEDIFFYDRERLIKSRITANGGESRADITSPAKERHYLDOW
TWERPYPTISBYGGSSRYTIHYYDORPERLIKSRIAPARAKOFTHYGENSTITOR
TORDANSTSNIPKYDGGANNYALANDAYOGELDVIROYARHIGSYGSSBADE
STRSIBEVYJSLINGSPOTKLMKARVPAAGRTKLEREITNNSYTKWHEICSTNSSG
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VMFVGLGSPUERKPOLVPSMLIIRRKGYKRALVCAATFRAARDGLKQMATKSKIP
YKGSYGGSPURKAIANGSVDRRKKENCOLLIUOTSGRHKQQAELPEBMRQISEAFKPOL
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/db_xen_id="BAB10765.1"
/fb_xensia.ion="MBXXXXEBBHHHQQQQQQXEIXATETKIEQEQBQBQXQEISQAS
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/product="won"Hippel-Lindau binding protein (VHL binding
protein; VRP) _lke*___
                                                           evidence=not experimental
product="SRP54 (signal recognition particle 54 KDa)
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/db_xref="G1:10177617"
                                                                                                                                                                                                                                    'protein_id="BAB10763.1"
                                                                                                                                                                                                                                                                                                       db_xref="GI:10177616"
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GTISGENNDETWGTRISYBDAKUGFBEDEFULTEPPERSEGNGODDGLMKDVF
KVNDSCORRLASYGDLKSYMBAGIATDDETKSHTRLAGGDADGVSPPGLIKTEGG
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/procent id="Bandor1."
/db_xref="G1:10177615"
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SFGHSSVDAVVSSFLSGQRCVPLQEDTKEMREDVAICLSRTNLGLGFWMNNESLNKSE
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NTTTICCVPDELPANSNEIVGISPNPLIMLEKKKSQIEEKFEKEWQVSVTRIENEATS
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113545. .13545,13756. .13994,13988. .14138,14676. .14830,
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/note="gene_idikGM13.4"
                                                                                                                                                                                                                                            Structural analysis of Arabidopsia thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty pr and TAC clones
DNA. Res. 7 (1), 31-63 (2000)
                                                                                                                      Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E., Kotani,H. and Tabata,S.
eurosids II; Brassicalen; Brassicaceae; Arabidopsis.
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5957. _6439
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/codon_start=1
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complement (join (39873. .40058,40363. .40558,40657. .40754))

CDS

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Submitted (100 MRR-2001) Sanger Centre, Hinxton, Cambridgeshire, Call Sah, UK. Email enquirites: humquery@angor.ac.uk Clone requests. Clonerequestosanger.ac.uk clone mar 12, 2010 this sequence version replaced gi:1255648.

On Mar 12, 2010 this sequence version replaced gi:1255648.

During sequence assembly data is compared from overlapping clones. Where differences are found these are amotated as variations together with a note of the overlapping clone name. Note that the variation amotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with mix a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequencial problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, Sw.,
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Human DNA sequence from clone RP13-192B19 on chromosome Xq24-25,
    Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Bases 1 to 10920)
                                                                                                                                                                                                                               Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                         Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the pirap assembly program
All manually edited bases have been reduced to quality zero.
Quality ievels above 40 are expected to have less than
1 error. In 2,000 bp.
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/clone="CTD-2330P21"
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/db_xref="taxon:9606"
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                                                                                           /evidence=not_experimental
/protein_id="BAB10767.1"
/db_xref="G1:10177620"
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/protein_id="BAB10769.1"
/db_xref="GI:10177622"
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/note="gene_id:K6M13.11
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/note="gene_id:K6M13.9
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DOE Joint Genome Institute.
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8347. .38588
mote="TIGGERI repeat: matches 2202. .2417 of consensus"
8578. .38736.
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noce="LIPA12 repeat: matches 5857. .6018 of consensus"
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44766. .44960
fore="ILMC3 repeat: matches 7525. .7735 of consensus"
note="LiMD3 repeat: matches 7588. .7734 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1MD1 repeat: matches 6073. .6218 of consensus"
8732. .28768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LIMD1 repeat: matches 5530. .6073 of consensus"
3604. .33953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Tigger2a repeat: matches 15. .434 of consensus"
9854. .39942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LIME3 repeat: matches 5782. .6140 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Ally repeat: matches 1. .309 of consensus"
1793. .41915
note="LIME repeat: matches 5495. .5618 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="LTRIGA repeat: matches 225. .438 of consensus"
1475. .41791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="TIGGER1 repeat: matches 1. .157 of consensus"
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100es=11,1913 repeat: matches 6034. .6156 of consens
12974. .43076
10ces=WERSA repeat: matches 11. .109 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="THELA repeat: matches 1. .354 of consensus" 5764. .36123 mote="WILLAL repeat: matches 1. .365 of consensus" 7297. .37346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9330. .39394
note="MER8 repeat: matches 177. .236 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1 repeat: matches 3685. .4337 of consensus"
8347. .38588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MLT1A1 repeat: matches 1. .365 of consensus"
                                                                                                                                                                                                note="MER2 repeat: matches 106. .210 of consensus"
                                                                                                                                                                                                                                                                                           note="L1PA3 repeat: matches 8. .6146 of consengus"
                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 258. .515 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Alusx repeat: matches 1. .305 of consensus" 8584. .28731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MLT2A repeat: matches 1. .453 of consensus"
9294, .39327
                                                                                                                                                                                                                                                                                                                                             note="MSTD repeat: matches 1. .343 of consensus"
17656. .27719
"hote="12-copies 2 mer aa 95% conserved"
17970. .38213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER3 repeat: matches 20. .56 of consensus"
8769. .29267
                                                                                                                                                note="L1PA16 repeat: matches 6107. .6157 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="LiME3 repeat: matches 5616. .5704 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="17 copies 2 mer ac 100% conserved" 9330. .39394
                                               note="MER92A repeat: matches 1. .412 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="23 copies 2 mer ta 78% conserved"
0499. 40878
                                                                                       /note="28 copies 2 mer aa 71% conserved"
19858. .19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7297. .373mo
note="25 dopies 2 mer at 72% conserved"
                                                                                                                                                                                                                                               note="LTR24 repeat: matches 1.
0988. .27142
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/note="HALL ;
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SWISSPROT, TE:, TREMBL, WP:, WORMPEP; Information on the WORMPEP database can be found at the found contigs of human chromosome X, constructed by the Sanger Centre Chromosome X mapping Group, Purther Information can be found at
                                                                                                                                   http://www.anger.ac.uk/MGP/CDMX
RP13-132819.s from the library RPC1-13.1 constructed by the group
of Pieter & from the library RPC1-13.1 constructed by the group
of Pieter & from the library RPC1-13.1 constructed by the group
of Pieter & Banca.
http://www.chori.org/bacpac/home.htm
btcp://www.chori.org/bacpac/home.htm
btcp://www.chori.org/bacpac/home.htm
rpc.nor.
RP13-192819.1 tm any be shorter because we sequence overlapping
the true left end of clone RP13-192819 is at 1 in this sequence.
The true left end of clone RP13-192819 is at 1 in this sequence.
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'note="LiPBa repeat: matches -1540. .-1343 of consensus"
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2842. .13027
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3463. .15156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1ME3 repeat: matches 4890, .5984 of consensus"
072. .9376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1669. .11758
note="LIMC5 repeat: matches 7132. .7221 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PBa repeat: matches -942. .1930 of consensus"
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16395. .16539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="LIM4 repeat: matches 3554. .4429 of consensus"
270. .6579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MLT1C repeat: matches 432. .466 of consensus"
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'note="MLT1A1-internal ropeat: matches 1. .1063 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluJo repeat: matches 1. .304 of consensus"
603. .6774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSx repeat: matches 1. .305 of consensus"
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2500. 12578
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75. .468
hote="97 copies 2 mer tt 57% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="17 copies 2 mer gt 88% conserved" 0105. .10493
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .109920
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
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/clone="RP13-192B19"
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on the WORMPEP database can be found at http://www.sngar.ca.u/k/Projecs0/Calegans/wormpep RP4-569D19 is http://www.sngar.ca.u/k/Projecs0/Calegans/wormpep RP4-569D19 is from the library RCCL-4 constructed at the Roswell Park Cancer Institute by the group of Peter de Jong. For further details see http://bacper.cmd/buffalo.edu/
NECTRANT: This sequence is not the entire insert of clone RP4-569D19 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone RP4-559D19 is at 1 in this sequence. The true right end of clone RP4-559D19 is at 31286 in this sequence. The start of this sequence overlaps with sequence AL009049.
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10508. .10592
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294. .7605
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'note="AluYa5 repeat: matches 150. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5999. .6140
/note="AluSq/x repeat: matches 1. .136 of consensus'
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[643. .2088
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'note="L2 repeat: matches 2625. .2704 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSc repeat: matches 61. ,304 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1206. .4486
/note="Alujb repeat: matches 1. .282 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thote="AluSx repeat: matches 1. ,312 of consensus" 1786. .8087 fnote="AluSg repeat: matches 6. ,307 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .205 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .258 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .237 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4747. .4858
/note="MIR repeat: matches 47. .163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluY repeat: matches 1. ,300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8910. .8965
/note="28 copies 2 mer at 100 conserved"
complement(9476, .9902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1966. .5077
/note="MIR repeat: matches 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MIR repeat: matches 151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 1929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L2 repeat: matches 2470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (9476. .9902)
'note="match: GSS: Em:AQ222044"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP4-569D19"
/clone="lb="RPCI-4"
805. .1011
/note="MIR repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .918. .4117
'note="MIR repeat: matches 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="match: GSS: Em:AQ061599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :omplement(9546. .9904)
'note="match: GSS: Em:B57571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3277. .8661
/note="match: STS: Em:R85597"
                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           'chromosome="22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453. .7182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        012, 1253
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                                                                                                                                                                                                                                                                                                                                                        FEATURES
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emi. EMBL; Sw.; SWISSERDY; Tr.; TREMBL; Wp.; WORMPEP; Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of Munan chromosome 22, constructed by the Sangar Centre Chromosome 22 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
                                                                                                                                                                                                                                                                                                                                                                              note="HUERS-P3b repeat: matches 3164. .3360 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear PRI 12-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On bec 2, 1999 this sequence version replaced gi.3445463.
This sequence has been finished according to sequence map criteria as tollows. An attempt is made to resolve all sequencing problems, such as compressions and repeats but not necessarily within known amnoted things repeat sequence elements (e.g. Alu), where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains 3' part of a novel gene similar to mouse Ras, swamethasone-induced I (Ras-related protein, RASDI, DEKRASI) and the last exon of the MB gene for Myoglobin, ESTB, STSs and GSSBn,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; CpG Island; Dexamethasone-induced; DEXRAS1; Myoglobin; RASD1
Homo sapiens.
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                                                                                                                                                                                              repeat: matches 5835. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OB-DEC-1999) Sanger Centre Hinxton, Cambridgeshire, CEDO 15A, UK. B.mail enquiries: humquery@sanger.ac.uk Clone requeste: clonerequesteste@sanger.ac.uk
                             // Arce="LiM4 repeat: matches 4543. 5384 of consensus"
5/53. 45860
// Arce="LiM4 repeat: matches 2467. 2575 of consensus"
7850; 4550
// Arce="LiM4D repeat: matches 104. 836 of consensus"
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Human DNA sequence from clone RP4-569D19 on chromosome 22q13.1
                                                                                                                                                                                                                                                                                                                                                                                                    48364. .51335
/note="LTR25-internal repeat: matches 3736. .6713 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                              note="MER61B repeat: matches 1. .396 of consensus"
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/note="MER61-internal repeat: matches 742. .4550 of
                                                                                                                                                                                                                                                                       7452. .48284
note="MEK61-internal repeat: matches 1. .2371 of
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                                                                                                                                                             46717, .47044
/note="L1MB4 r
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52506. .52906
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HS569D19/c
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KEYWORDS
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ò 셤 COMMENT

/replace="gtg" repeat_region 2563726574 repeat_region 2687269688	Anotes - Markeyas: Marches 4.1. 123 Oil Consensors Variation 26955. 26937  Anotes - Markey 189-824119; tct in this entry; substitution* Anotes - Markey 189-824119; tct in this entry; substitution*	variation 27020. 27022 variation 27020 variation variation 27020 variation v	variation 27055. 27057 /note="clone RP5-824119; atg in this entry; substitution /note="clone RP5-824119; atg in this entry; substitution	/replace="agg" variation 2708427086	10.5%; Score 19; DB 9; Length 114771; 100.0%; Pred, No. 12;	9; Conservative		DD 62214 TGGTGATGGAATGTT 62196	RESULT 29 AC097300	ž	***, 54 unordered pieces.		Σ	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Rodentia; Sciuroquathi; Muridae; Murinae;	Rattus. Rattus 1 (hame 1 to 120531)	AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,	Barbaria, J. Benton J. Pilange, K. Blankenburg, K. Bonnin, D., Ranke J. Powie, S. Briowa, M. Brown, E. Brown, M. Bryant, N.P.	Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T. F., Carter, M. Cavazos, S. B., Charko, J., Chavez, D.	Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,	Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,	Douthwaite, K.J., Draper, H., Dugan-Nocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,	Gabiei, Perraguco, D., Flagg, N., Fotc, J., Foster, F., Galiez, F., Garcia, A., Gao, J., Garcia, Garcia, N., Gill, R.,	GOLTELLO, M., GURVARA, M., GURARALO, MATCHO, MATCHO, MATCHO, MATCHO, M., Hernandez, O., Harrandez, O., Hornse, M., Holloway, C., Hollis, B.,	Homel, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,	Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Krarovic, J., Kurehi, B., Landry, N., Leal, B., Lewis, L.C., Lewis, L.	Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Loulseged, H. Lorado B. T. M. Turcier B. Lurrier B. Luna R. Ma. J.	Maheshwari, M. Mayua, P. , Martin, R. , Martindale, A. , Martinez, E. , Marcon M. Martinez, E. , Marcon M. Markov M.	Miner (2) Miner (2) Mitchell T., Mohabbat (2), Morgan, M., Morris, More M. Man (3) Moharen I. Mohren M. Minyen A. Mouven M.	Nguyen, N. Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraquinye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peerez, L.,	Petera, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,	Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
1059311608 /note="Link4 repeat: matches 52656298 of consensus" 179812082 /note="LinkEl repeat: matches 60106156 of consensus"	142/5121/7 // notes="seq"   FPS-824119; atg in this entry; substitution"   Fppaces="seq"   Fppaces"   Fppaces   Fppaces	/most="1187" repeat: matches 55766016 of consensus" 1343111736	//UCC==ALLASA Tepeal: Matches 1000 of Consensus 1379214127 /note="LTR9 repeat: matches 10290 of consensus"	1412814415 /note="AluSx repeat: matches 1289 of consensus"	1441614720 /hote="LTR9 repeat: matches 290612 of consensus" 1400915033	/note="FLAM C repeat: matches 2126 of consensus" 15.08315640	/note="L2 repeat: matchus 21572743 of consensus" 1561715787	/note="MIR repeat: matches 85. 261 of consensus" 16487. 16510 /note=#12.con168 2 mer ct 100 conserved"	16658. 16913 /note="march: GSS: Em.813882"	17863	18408 . 18441 /note="17 conies 2 mer at 97 conserved"	1841718422   Incre="close RD5-824119: tatata in this entry: insertion"	/replace=rg" 1868619065	/note="MLT1J repeat: matches 1398 of consensus" 1928619459	/note="MERSA repeat: matches 16188 of consensus"		19703: .1903. /note="Aludo/FRAM repeat: matches 164285 of consensus" 1907. 19014	/note=": 12521   for the construct	/Jocte="close RP5-824119; gtgt in this entry; insertion" /replace="qt"	1991720520 /note="L2 repeat: matchos 18772592 of consensus"	2059920618 /note="L2 repeat: matches 25842624 of consensus"	2119621503 /note="AluJo repeat: matches 1305 of consensus"	21/9821922 /note="Flam" C repeat: matches 1125 of consensus" 	/note="Alusx repeat: matches 1312 of consensus" 22448 22683	/note="68 copies 2 mer to 61 conserved" 2558 2007	/note=122 copies 2 mer ct 81 conserved"	/rote="Alujb repeat: matches 1312 of consensus"	234252373/ /note="Alusg repeat: matches 1292 of consensus" 22703 24646	20,23: .tarts 20,05: .matches 7262 of consensus" 2418924357	/note="MIR repeat: matches 47220 of consensus" 2607626159	/note="MIR repeat: matches 59144 of consensus" 2645126453
repeat_region repeat_region		repeat_region	repeat_region		repeat_region		repeat_region	repeat_region	misc_feature	repeat_region	repeat_region	variation	repeat region	repeat region	moiner treater	Topode Topode	repear_region	יים ביים ביים ביים ביים ביים ביים ביים				repeat region	repeat_region	repeat region	ropost teodor	epear_region	repear_region	repear_region	repeat_region	repeat region	variation

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NOTE: This is a "working draft' sequence .it currently consists of $4 contigs. The true order of the pieces is not known and their order in this sequence record is
Tanney J. Taylor C. Taylor T. Telfred B. Thomas, N. Thomas, S., Usmani, K. Vagquez, L. Vera, V. Villalon, V. Vinson, F. Mang, C. Mang, M. V. Villalon, V. Vinson, F. Mang, C. Mang, M. Millanson, A. Willanson, A. Willanson, A. Willanson, A. Willanson, A. Willanson, A. Woden, S. Worley, K. Wolch, W. Y. W. Millanson, A. Willanson, A. Willanson, A. Willanson, D. Williamson, D. Willa
                                                                                                                                                                 Direct Submission
Submitted (14-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Worley, K.C.,
                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12-2012) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plazar Houston, TX 77030, USA
On 11, 11, 2002 this sequence Version replaced gi:17064442.
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Center clone name: CH230-16435
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Submitted (04-AUG-2000) Human Genome Sequencing Center, Department
of Wolcentar and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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On Jun 17, 2002 this sequence version replaced gi:20335729.
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Web site: http://www.hgsc.bcm.tmc.edu/
Drafting Center Code: BCM
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                         AC078804.7 GI:21431061
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Shamiteed (04-DEC-1999) Production Sequencing Facility, DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases I to 129318) to 129318) To 1000 Joint Genome Center.
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10.5%; Score 19; DB 9; Length 129339;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0:
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www.shgc.stanford.edu
Ganliky: Phrap Quality >=40 99.44 of Sequence;
Bernated Total Number of Errors is 0.7.
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AC016597.4 GI:8573019
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                                                                                110176:
                                                                                                                                   115200:
                                                                                                                                                                                          120531:
                                                          107233;
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104325
104425
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                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
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---- Project Information Center project name: HBTN Center clone name: RP11-489M17 Center Summary Statistics Contact: hgsc-help@bcm.tmc.edu

AC078804 164456 bp DNA linear HTG 19-JUN-2002 Home sapiens chromosome 3 clone RPI1-489M17, WORKING DRAFT SEQUENCE, 7 inordered pieces.

LOCUS

RESULT 31

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AC078804

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Davila, M. L., Davis, C., Davy-Carroll, L., Dederich, D. A.,
Delanay, K. R., Delgado, D., Denn, A.L., Dingy, V. Dinhi, H. H.,
Douthwaite, K. J., Draper, H., Dugan, Rocha, S., Dubhin, K. J.,
Barnhart, C., Edgar, D., Edwards, C., Elbaj, C., Escotto, M.,
Ralis, T., Pergaduto, D., Edwards, C., Elbaj, C., Escotto, M.,
Gabrsin, A., Gao, J., Garica, A., Darner, T., Garza, M., Hennaider, J.,
Harris, C., Harris, M., Harlak, P., Hale, S., Hamilton, K.,
Harris, C., Harris, M., Harlak, P., Hale, S., Hamilton, K.,
Harris, C., Harris, M., Halber, J., Hume, J., Jackson, L. E.,
Jacobson, B., Jai, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kalay, Y., Mulyk, S., Hume, J., Jackson, L. E.,
Jacobson, B., Mari, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kalay, K., Man, M., Leal, B., Lewis, L. C., Lewis, L.
Kratlsson, E., Kalay, Y., Mulyk, S., Marina, R., Marina, R., Marina, R.,
Massey, E., Man, Mayue, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mahinay, E., Wiched, M. P., Martina, R., Martindale, M., Mayuen, N.,
Mosterson, E., Nawkenon, J., Newtoon, N., Nguyen, A.,
Moster, M., Nickerson, E., Newtenon, N., Nguyen, N.,
Oregunye, M., Oricdo, R., Pecce, A., Peptron, B.,
Rives, A., Rojubokan, I., Shoohtari, N., Stone, H.,
Rives, M., Rojas, A., Rojubokan, I., Shoohtari, N., Stone, H.,
Scherer, S., Scott, G., Shen, H., Shoohtaria, N., Stone, H.,
Taneey, J., Taylor, C., Taylor, T., Taneey, J., Ward, M., Mari, S., Marchell, M.,
Marins, G., Marchell, M., Marins, M., Marins, S.,
Ward, M., Marins, M., Ward, M., Ward, M., Ward, M., Ward, M., Marins, S., Marchell, M., Marins, S., Marchell, M., Marins, S., Marchell, M., Ward, M
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NOTE: This is a "working draft's sequence. It currently
consiste of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
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Submitted (108 MV).
Submitted (108 MV).
Bulletted (108 MV).
Bullette
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On Jul 11, 2002 this sequence version replaced gi:17973833.
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Center project name: GTNP
Center clone name: GTNP
Center clone name: GTNP
Sequencing vector: planning
Centering vector: planning
Centering vector: planning
Assembly program: Phrap; version 0.990329
Consensus quality; 10374 bases at least quo
Consensus quality; 114597 bases at least Q00
Consensus quality; 114597 bases at least Q00
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Contact: hgsc-help@bcm.tmc.edu
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Unpublished
2 (bases 1 to 164995)
Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACUSEY) 164995 bp DNA linear HTG 12-JUL-2002 Rettus norvegicus clone CH230-178A23, *** SEQUENCING IN PROGRESS ACCESS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                       Chamistry: Dye-primer Bodipy: 75% of reads
Chemistry: Dye-primer Bodipy: 75% of reads
Chemistry: Dye-terminator Big Dye: 22% of reads
Consensus quality: 18577 besse at least Q40
Consensus quality: 18577 besse at least Q40
Consensus quality: 16039 bases at least Q20
Estimated hisert Base: 165132; sum-of-contigs estimation
Daality coverage: 5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7694: contig of 7694 bp in length 1799; gap of unknown length 16259; contig of 856 bp in length 16259; gap of unknown length 13239; contig of 14960 bp in length 21329; contig of 14960 bp in length 52312; contig of 20073 bp in length 78975; contig of 20073 bp in length 78975; contig of 2663 bp in length 78975; contig of 2663 bp in length 118077; contig of 2663 bp in length 118077; contig of 18922 bp in length 118077; gap of unknown length
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/db_xref="taxon:9606"
/chromosome="3"
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Joint Concernation Production Sequencing Pacility, DOE Joint Janoha (10-207-2010) Production Sequencing Pacility, DOE Joint Janoha (10-207-2011) Production Sequence Office of 2, 2001 this sequence version replaced gi:14522976.

This entry has been amnoated with sequence quality setsimates computed by the Phrsp Assembly program.
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Massey, E., Mawhiney, E., Ncieod, M. P., Meador, M., Nei, G., Metzker, M., Milar, G., Miner, Z., Mitchell, T., Nohabbat, K., Moorala, M., Moorie, S., Moser, M., Nickerson, J., Newtson, N., Mguyen, A., Nguyen, A., Nguyen, N., Nickerson, E., Newtson, N., Oghi, M., Okwonno, G., Oviedo, B., Patch, A., Payton, B., Peerry, J., Perers, L., Pitkens, R., Primas, B., Pill, L., Oullas, M., Ren, Y., Rives, M., Rojas, A., Rojubckan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoosherri, M., Stoosh, H., Stoosherri, M., Stoosh, M., Soosherren, S., Scott, G., Shen, H., Shoosherri, M., Stoosh, H., Stoosherri, M., Stoosh, H., Shoosherri, M., Stoosh, M., Shoosherri, M., Stoosh, M., Shoosh, M., Shoosherri, M., Wangor, C., Taylor, T., Telfrod, B., Thomas, M., Thomas, M., Wangor, M., Wangor, C., Walliamson, A., Warren, R., Wangor, M., Wangor, M., Walliamson, A., Wieczyk, R., Rodon, S., Warren, R., Wangor, M., Walliamson, A., Wieczyk, R., Rododen, S., Warren, R., Wangor, M., Wu, K., Wi, F., Zorrilla, S., Nelson, D., Weistok, G., McLisock, G., and Gibbs, R., Weinstock, G., and Gibbs, R.
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NOTE: This is a "working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as trues of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as sesones it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Jenentics, Baylor College of Medicine, One Baylor Plaza, Houeton, TX 77030, USA
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Center project name: GYAG
Center Clone name: GYAG
Center Clone name: GYAG
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Center Clone name: GYAG
Generic Popt-terminator BAG
Assembly program: Phrap, version 0.990229
Consensus quality: 103378 bases at least QAO
Consensus quality: 16592 bases at least QAO
Consensus quality: 122256 bases at least QAO
Consensus quality: 122256 bases at least QAO
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This entry has been amnotated with sequence quality
estimates computed by the Pinapa assembly program.
All manually edited bases have been reduced to quality zero.
Quality leads above 40 are expected to have less than
1 error in 10,000 bp.
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                                                                                                                       Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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NOTE: This is a "working draft' sequence. It currently consists of 5 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigg are represented as truns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Scherer'S. Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, B., Sonaike, T., Sparke, A., Stanley, H., Stone, H., Sutton, A., Stanley, H., Stone, H., Stanley, S., Wather, B., A., Tahor, P., Tahor, P., Tahor, P., Tahor, P., Tahor, S., Thomas, M., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, G., Walliagor, S., Wathington, C., Walliagor, S., Williams, G., Williams, C., Wu, Y., Washington, C., Wallington, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                Direct Submission
Submitteed (19-ULL-2002) Human Genome Sequencing Center, Department
of Wolecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dyo; 100% of reads Assembly program: Phrapy version 0.99029 Consensus quality: 12210 bases at least 040 Consensus quality; 140812 bases at least 030 Consensus quality; 140812 bases at least 0
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// note assembly_name:Contig108", 15873, 18136

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// note assembly_name:Contig1112", 18277

// note assembly_name:Contig113", 18277

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3735. 3970.

700e="assembly_name:Contig119"

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/db_xref="taxon:9606"
/chromosome="17"
/clone="RP11-68105"
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ACOG6281 199551 bp DNA linear HTG-12-AUG-2000 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROFESSES ***, 2 unordered places.
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Homo sapiens chromosome 10 clone RPI1-536J24, complete sequence.
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Submitted (09-JUN-2000) Genome Therapeutics Corporation, 100 Beaver
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Smith, D.R.
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Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
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Live 0; Mismatches 0
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/db_xref="taxon:9606"
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2 (bases 1 to 185754)
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Matches 19; Conservative
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KEYWORDS SOURCE ORGANISM	HTG; HTGS PHAGE1. Plasmodium falciparum. Plasmodium falciparum.	PUBMED 91. REFERENCE 3 AUTHORS BO	9110172 Solvaces I to 251199) Boyeen, C. Inyoul, L., Smith, T.M., Smit, A., Wang, K., Rowen, L. and
REFERENCE	Eukaryota: Alveolata; Agicomplexa; Haemosporida; Plasmodium. 1. (bases 1 to 19951) Urman bu Binn E I. Ain P. Dowlay, D. Man J. Tamaki T.	TITLE T-I	Hood.L. Hood.L. Receptor Alpha Delta Locus Complete Nucleotide Sequence Annual Jahod
TITLE	nyman, k.m., rung, b.m., vin, r.m., rav, b., rav		This citation covers bases 1-983545 and bases 1064020-1071650 4 (bases 1 to 251199)
JOURNAL	Unpublished 2 (bases 1 to 199551)	AUTHORS BO	Boysen, C., Lee, I., Smith, T.M., Smit, A., Kai, W., Lee, R. and Leroy, H. Direct, Submission
AUTHORS	Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W. Direct Submission	JOURNAL Sul	Submitted (20-JUL-1997) Department of Molecular Biotechnology, University of Washington, Box 357730, Seattle, Washington 98195,
JOURNAL	Submitted (05-JAN-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA	USA REMARK Com	USA Complete nucleotide sequence of the human T-cell receptor alpha addra lower
COMMENT	on Aug 12, 2000 this sequence version replaced gi:8810457.  * NOTE: This is a "working draft "sequence. It currently consists of 2 contigs: The true order of the pieces is not known and their order in this sequence record is	COMMENT OF	On Jun 12, 2001 this sequence version replaced gi:2766593. Sequencing method: high redundancy shoughn. Incerpersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.ed/RW/RepeatMasker.
	<ul> <li>russ of M, but the exect sizes of the gape are unknown.</li> <li>ruth record will be updated with the finished equance.</li> <li>secon as it is available and the accession number will.</li> </ul>	hti FEATURES SOURCE	p://sersc.nbr.washington.edu/-chrisa/software/sputnik.html). Location/Qualiffers 125:139 Hinterson
9 9 1	• De pieserveu.  1 14526: contig of 41526 bp in length • 41527 41726: gap of unknown length • 4127 19555: contig of 157825 bp in length.	source	/Organisms = Now equations /Ob xref=""t axon: 9606" 33706 138937 /Organisms = Homo sapiens" /Ah xref="t axon: 9606"
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	/clone="PPYACBB-95" /clone="3D7"	repeat_region	
BASE COUNT	83197 a 17543 c 19759 g 78852 t 200 others	repeat_region	
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Best Local	%; Pred. No. 12; 0; Mismatches (	gene	4449
	2000 64	promoter	44494468 //mana=#T/CD81/521#
	ATTTTATTACTTATATGG	mRNA	/ Standard name "TCRANSSI" / Anote = 101 join (= 4647 name TCRANSSI" / Anote = 1018 (= 1647 name 1018)
RESULT 39 HUAE000659 LOCUS		CDS	/groduct="TCRAVSS1" /note="0ld name TCRAVISS1" joint(467 4698,4875>5162) /enne="TCRAVS1"
ACCESSION	SOURTO (section 2 of 5) of the Complete Nucleotide Sequence. AROUGES9-AROUGES1 UBS199 AROUGES9-1 GT:2258025		/grandard name="TCRAVISG1" /note="001 name TCRAVISG1" /codon_grant=1;;;;
SOURCE ORGANISM			/product=1.txxvss1. /product=1.txxvss1. /product=1.txxvss1. /db.xref==[9]:1338902.1"
REFERENCE	bukaryota; metazoa; thotuata; transaaa; vertentata; butereostomin; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (baees 1 to 221199)		Y LEGISLAGI JOHN TRATAGESTELBINGAGDEN ANGELY MAGNET LEV KREGESS VINCI. YTDSSSTYLYWYKQEPGAGLQLLTY IFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQT GDSAI YFORES
AUTHORS	Koop, B.F., Rowen, L., Wang, K., Kuo, C.L., Seto, D., Lenstra, J.A., Howard, S., Shan, W., Deshpande, P. and Hood, L.	V_segment	join(4647. ,4690,4875>5162) /gene="TCRAV5S1"
TITLE	The human T-cell receptor TCRAC/TCRDC (C alpha/C delta) region:		
MEDLINE	Genomics 19 (3), 4/8-493 (1994) 94245236 8188290	misc_recomb	D 5.63. 5.68 /gene="TCRAV551" /standard name="TCRAV551"
REFERENCE AUTHORS	This citation covers from bases 966383-1064019 2 (bases 1 to 251199) and Boysen, C., Simon,M.I. and Bood, L.	misc_recomb	
TITLE JOURNAL MEDLINE	Analysis of the 1.1-Mb human alpha/delta T-cell receptor locus with bacterial artificial chromosomo clones denome Res. 7 (4), 330-338 [1997] 97264339	misc_recomb	/standard name="TCRAV5S1" /noce="spacer" b 51315201 /gene="TCRAV5S1"

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Brassico pasubap, Oleifera DNA for reverse transcriptase gene of Line Reconsidents, 12141-07.
MAY 1960.1 GI:18564974
MAY 1960.1 GI:18564974
MAY 1960.2 GI:18564974
MAY 1960.2 GI:18564974
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MAY 1960.3 GI:18564974
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Submitted (10-CT-2001) Alix K., Biology, University of Leicester,
University Road, LEI 7RH, UNITED KINGDOM
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alix, K., Ryder, C., King, G. and Heslop-Harrison, J.S.
The genemic organization of retroelements in Brassica oleracea
Unpublished.
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1927. .31981
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2185. .32727
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                                       rpt family="MIR"
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             .26302
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(db_xref="Gf:1358027"
Trenslatei="MESFLGGUZ""
THYSPAYLQWYRQDFGRGFVFLLIRENEXERRKERLKVTFDTTLKOSLFHITAGQP
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5650...5724
                                                                                                                                                                                                                                                                                                                                complement (8895, .9195)
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10101. 11383
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Mamnalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Optinicermes. Cyprinidae; Danio.

Shindon; Krapalk, E. M., Ziniti, J., Sim C., Yamada, E., Kaplan, S., Jackson, D., de Sauvage; F., Ostoch, H. and Pishman, M.C., Zebratish genetic map with 300 microsatellite markers

9303038 (3), 219-222 (1999)
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Cardiovascular Research Center
Messachusette General Hospital
Mail code 1949100A, 149 11th Street, Charlestown, MA 02129, USA
Fax: 617265806
Email: fishmanseph.cruccharvard.edu
http://zebrafish.mgh.harvard.edu
primer A. GTTGGGTTGANACNGTTGGG
Primer B. TGGAMGGATCATCTGANCCC
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LOCUS

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Direct Submission
Submitted (15-NOV-1993) Guylaine Lepine, Oral Biology, University
Of Florida, 1600 SN, Archer Road, Gainesville, Florida, 12610-0424, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tränglation="MTAELFSFSRLONLEHYRPAKNVLTLCRTANLAKLNPKLPELEK
AIEMEDLALNPPVANELTPOVIALDEBRDRAYOALMSRVRSYAFDEDSOLRNAAARIE
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NRRALLARRASYGEAAVEKNERALIAENLRPLILAR I VEEKKTAVFAGRILGTGKNRHYL
ITFVARNOEDERDRWYRINGGOLYVV PEDELPRPKKKKKRASSTDTPSEBPVI-DBOSQG
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Progulske-Pox.A., Tumwasorn,S., Lepine,G., Han,N., Lantz,M. and
Patti,A.M.
Cloned portion-ones gingivalis genes and probes for the detection
of pariodonical disease
Location (basifiers
Location) Lalifiers
                                                                                                                                                                                                        /clone_lib="Hind III digestion of 381 chromosomal DNA in pUC18"-
                                                                                                                                                                                                                                                                                                                                                    function="Might be involved in the colonization process
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(1488-1507 and 1509-1528) "
(full 1507 and 1509-1528) "
(function="Putative transcription-termination signal"
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Thesis (1993) Oral Biology, University of Florida (bases 1 to 1841)
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                                                                                                                              1. .1841
/organism="Porphyromonas gingivalis"
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Sequence 5 from patent US 5824791,
AR049926.1 GI:5971918
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Pred. No.
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/clone="GL7"
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                                                                                                                                                                /strain="381"
                                                                                                                                                                                                                                                                                          /gene="hagC"
374. .1426
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Best Local Similarity 100.
Matches 18; Conservative
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                                 Lepine, G.
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-10_signal
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Pajingivalis hagC gene encoding HagC hemagglutinin protein.
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Listeria monocytogenes ATCC 19115.
Lateria: Firmicutes, Bacillales, Listeriaceae; Listeria.
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-259 c 225 g 301 t
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Porphyromonas ginglyalis.
Porphyromonas gingivalis
Bacteria; Bacteroidetes; Bacteroides; Bacteroidales;
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Patent: WO 0228891-A 1611 11-APR-2002;
Pasteur Institut (FR)
                                                                                                                                                                                                          DB 9;
49;
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Sequence 1611 from Patent WO0228891.
AX414620
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                                                                                                                                                                                                        5.9%;
| Similarity 100.0%;
18; Conservative 0
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                                                                                                             493. .>750
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BASE COUNT 464 a 507 c 471g 399 t
ORIGIN
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Beet Local Similarity 1007s, Pred No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels
Oy 24 GCTGGAAGACGTCTTCG 41
Db 1627 GCTGGAAGACGTCTTCG 61
Db 1627 GCTGGAAGACGTCTTCG 610
Search completed: June 9, 2003, 12:33:20
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0; Gaps

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June 9, 2003, 08:36:50; Search time 474 Seconds (Withbur alignments) 1289:365 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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LEBSKATTHENIGDAAPRASP
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//ocdon_state_al
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/hote="minK.related peptide 1, Thr substituted for Ile at
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74...445
/note="mink-related peptide 1, Thr substitued for Met at amino acid 54"
                                                                                                                                        Homo sapiens
Bikaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Futheria; Primetes; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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153 c 157 g 201 t
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100.0%; Pred. No. 67;
iive 0; Mismatches 0; Indels
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Polymorphisms associated with cardiac arrythmia Patent: WO 0222875-A 5 21-MAR-2002;
YALE UNIVERSITY (US)
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/db_xref="taxon:9606"
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//pcref=16.10.10.5310.1"
/db_xref="G1:21419815"
/translation="WASTISHTQTLEDVFRRIFITYHDWHROWTTAEOEALQAKVDAE
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NFYVILYILAWHAGWESEIIYALLVSTVRSKRREHBNDPYHGYIVEDWGEKYKSOLLN
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                                                                                                                                                                                                                 /note="minK-related peptide 1, Val substitued for Ala at amino acid 116"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/codon start≃1
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Sequence 3 from Patent WO0222875,
AX406941. GI:21439816
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                           /organism="Homo sapiens"
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/tränslation="MSTLSNFTQTLEDVFRRIFITYMDWRQNTTAEQBALQAKVDAE
NEYYVLLILMWIGHESTIVALIUSTYKSKRREHSNDPYHQYIVEDWQEKYKSQLLN
LEBERATTHBXIGAAGFRASP
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The sequencing project is supported by Japan Science Technology Research of the data (ACCESSION No. APD000165 - APD000173).
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Mammalia Euthoria; Primates; Catarrinii, Hominidas; Homo.
Hettorii, M., 1861, X., Toyoda, M., Tayotr, E., Hong-Seog, P., Fujisma, A., Yada, T., Totodi, Y. and Sakaki, Y.
Homo sapiens 24, 68bp genemic DNA of 21422.1
Published Only in Database (1999)
Hettorii, 18fii, X., Toyoda, A., Taylor, E.D., Hong-Seog, P., Hettorii, 18fii, X., Totoda, A., Taylor, E.D., Hong-Seog, P., Pijiyman, A., Yada, T., Totoki, Y. and Sakaki, Y.
                                  Bikaryota, Netazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammala, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 809)
Domenech, A., Setivilli, X. and de la Luna, S.
Cloning of human MRR1 cDNA
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Clone:01202, complete sequence.
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2. (hases 1 to 809)

Domenech, A., Estivill,X. and de la Luna,S.

Domenech, A., Estivill,X. and de la Luna,S.

Direct Shahnsasho

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Direct Shahnsasho

Directon Oncologica, Avia. de Castelldefels Km 2,7,

L'Hospitalet de Llobregat, Barcelona 08907, Spain

Location/Qualifiers
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/protein_id="AAG13416.1"
/db_xref="G1:10121888"
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/db_xref="taxon:9606"
/chromosome="21"
/map="21q22"
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Direct Submission (16-JUN-1998) Section of Developmental Biology and Biophysics, Department of Pediatrics and Boyer Center for Molecular Medicine, Yale University School of Medicine, 295 Congress Avenue, New Haven, CT 06536, USA
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Homo sapiens voltage-gated K+ Channel subunit MIRPI (KCNE2) mKNA,
AF90209.
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Homo sapiens minK-related peptide 1 mRNA, complete cds.
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Bukaryota, Mecazoa, Chordata, Craniata, Vertebrata; Euceleostomi, Namalia, Euchleria, Primates, Catarinii, Hominidae, Homo.

Bukaryota, Metazoa, Eucheria, Primates, Catarinii, Hominidae, Homo.

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Raticori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Homo sapiens 890, 2310p genomic DNA of 21q2.1 (REGION: D218226-AML CLOME RANGE: B2144P14-E5089)

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                                                                                                                                                                                                       APD00167 100000 bp DNA linear PRI 08-JAN-2000 How sapiens genomic DNA, chromosome 21922.1, D215225-AML region, Clome B2344R14-f50BB, segment 3/9, complete sequence.
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18 Hattori, M. Ishii, K. Tryoda, A., Shiba, T. and Sakaki, Y.
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19 Hattori, M. Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
19 Hattori, M. Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
19 United (11-MM-1998) Masahira Hattori, Kitasato University,
Department of Science, 30T Sequencing laboratory, Kitasato
1-15-10, Sagamhara 2-3, Japan (8-mailihattoridago.ims.u-tokyo.ac.jp.
This sequence is conducted by Kitasato University 38T sequencing
Laboratory as a Jost Sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: 481-3-549;5-562, Fax : +81-3-5449-5445,
sakakishço, ima u-tokyo.ac.jp
Sub-laader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D. The
sequence is submitted by:Human Gonome Sequencing in ALIS project of
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5-19 Yonbance and Technology Corporation (1871)
5-19 Yonbance of this decision of the sequence of the sequence of the sequence and relationship to other sequences please visit our sequence arehive Meb site (https://www.alis.tokyo.jst.go.jst.go.jpr.
or send email to webnaster@www.niis.tokyo.jst.go.jpr.
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         Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 9; Length 24608;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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/db_xref="taxon:9606"
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/chromosome="21"
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                                                                          Location/Qualifiers
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. 5420 c 5437
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Best Local Similarity 100.0%;
Matches 21, Conservative 0;
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

DEFINITION

AP000052

ACCESSION

BASE COUNT

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FEATURES

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Hartonia, Fujiyama, A., Taylor, F.D., Watanabe, H., Yada, T., Park, H.S., Toylor, A., Choi, D.K., Soede, E., Ohki, M., Taylor, T.D., Watanabe, H., Yada, T., Sakaki, Y., Taudian, S., Blechschmidt, K., Ohki, M., Marel, U., Deblar, J., Kudp, K., Kupe, K., Lehnann, M., Schudy, A., Patterson, D., Raichwald, K., Rump, A., Schillhabel, M., Schudy, A., Asakawa, S., Shintani, A., Sasaki, K., Nagamine, K., Witsuyama, K., Asakawa, S., Shintani, A., Sasaki, K., Nagamine, K., Witsuyama, S., Hornarakis, S., Minoshima, S., Shintau, N., Ordsisk, G., Scher, G., Scher, O., Deeario, A., Reschell, J., Kauer, G., Bloecker, H., Ramser, J., Beck, M., Klages, S., Hennig, S., Risseslmann, L., Decker, H., Ramser, J., Beck, M., Klages, S., Renselmann, L., Decker, H., Remer, J., Beck, M., Klages, S., Gorzym, K., Misseilo, D., Francie, P., Lehrach, H., Reinhardt, R. and Gardine, K., Nizetic, D., Francie, P., Lehrach, H., Reinhardt, R. and Gardine, K., Nizetic, D., Francie, P., Lehrach, H., Reinhardt, R. and Gardine, K., Nizetic, D., Francie, P., Lehrach, H., Reinhardt, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Attorney J. Voorda, A. Taylor, T.D., Watanabe, H., Yada, T., Chulasse, L., 1909da, A., Ishli, K., Torcki, Y., Choli, D.K., Soede, E., Obki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Obki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Belley, A., Meneal, U., Debbar, J., Kudpi, K., Lehnann, M., Schudy, A., Petterson, D., Reichwald, K., Rump, M., Schillabel, M., Schudy, A., Asamermann, W., Soenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shittani, A., Sasaki, T., Nagamine, K., Witsuyama, S., Hordischer, K., Baranti, P., Scharfe, M., Schoen, O., Desario, A., Hornischer, K., Baranti, P., Scharfe, M., Schoen, O., Desario, A., Hennig, S., Klesselmann, L. Dagand, E., Wehtmasyer, S., Botzym, K., dardine, T., Dagand, E., Wehtmasyer, S., Botzym, K., dardine, T., Dagand, E., Wehtmasyer, S., Botzym, K., dardine, T., Dagand, E., Mehrmach, H., Skilmardt, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10 ARR 2000) The Chromosome 21 Mapping and Sequencing Consortium: * RIKBN Genome Selecters Center.* Huann Genome Research Consortium: * RIKBN Genome Molecular Biotechnology, Genome Analysis * Koup * Institute of Molecular Biotechnology, Genome Analysis * GRP (Ed. University School of Medicine, Dept. of Molecular Biology * GRP. Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)
On May 30, 2000 this sequence version replaced gi:7717333.
On May 310, 2000 this sequence version replaced gi:7717333.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * GBF, Dept. of Genome Analysis, * Magnuschweig, Germany, * e.mail: * Magnuschweig, Germmany, * e.mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * RIKEN Genomic Sciences Center, Human Genome Research Group,
Sagamihara 228-8555, Japan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * Institute of Molecular Biotechnology, Genome Analysis, telechbergstrasses 11, D-07145 Jana, Germany,
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* UKL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Max-Planck Institute for Molecular Genetics,
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* e.mail: info-chtzl@molgen.mgg.de

* URL: http://chr21.rz-berlin.mgg.de/

AL163264: Submitted (10-Apr-2000).
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The DNA sequence of human chromosome 21
Nature 405 (6784), 311-319 (2000)
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* e.mail: nshimizu@dmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
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URL: http://hgp.gsc.riken.go.jp/
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JOURNAL
     REFERENCE
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                                Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
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each flanking site of PCR primers."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                     Mika Hirakawa, Japan Science and Technology Corporation (UST), Advanced Databases Department, 5-3, Yohancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mika@ackyo.jst.go.jp, URE:http://www-alis.tokyo.jst.go.jp/, Tarisla.1-3-214-8491, Pax:81-3-5214-8470)
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7221. .12320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori M., Ishii K., Toyoda A., Shiba T., Sakaki Y.;
"Homo sapiens 817,199bp genomic DNA of 21q22.1 GART and AML region";
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Mono Fapiens genomic DNA, chromosome 21g, section 63/105.
APO1119.1 G1:776871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japan Science and Technology Corporation (JST)
5-3, Yonbandro, Chiyoda-Ku, Toyo 102-0081 Japan
For further information about this sequence, including its
location and relationship to other sequences, please visit our
sequence archive Web site (http://www-alis.cokyo.jst.go.jp/HGS/)
or send email to webmaster@www-alis.tokyo.jst.go.jp/HGS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is conducted by Kitasato University JST sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sakakidego.ims.u-tokyo.ac.jp
Sub-leader: Tadayoshi Shiba Ph.D., Masahira Hattori Ph.D.
The sequence is submitted by Human Genome Sequencing in ALIS
project of UST.
                                                                                                                                                                                                                                                                                                               Submitted (15-APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                             Hirakawa M., Yamaguchi H., Imai K., Shimada J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory as a JST sequencing team.
Principal Investigator:Yoshiyuki Sakaki Ph.D.
Phone: +81-3-5449-5622, Fax : +81-3-5449-545,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Homo sapiens (human)
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source

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Query Match

Matches

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DEPINITION

ACCESSION KEYWORDS SOURCE

VERSION

RESULT 11

AP001719

ORGANISM

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ACO26481 99887 bp DNA linear HTG 30-MAR-2000
HOMO eaplens clone RP11-21E3, LOW-PASS SEQUENCE SAMPLING.
ACO26481
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/note='human solute carrier family 3, member 3, Accession
No. AF027153"
4392. 4746
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2. (beases 1 to 99887)
Birrelb B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9989); Birren B. Linton, L. Nusbaum, C. and Lander, E. Homo espiens, clone RP11-21E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismarches 0; Indels 0;
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Homo sapiens.
Homo sapiens
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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KEYWORDS
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Gaps ö 2105; gap of 100 bp in length 212879; cont.go of 774 bp in length 11755; cont.go of 776 bp in length 11855; cont.go of 769 bp in length 114624; cont.go of 769 bp in length 1747; cont.go of 633 bp in length 11417; cont.go of 633 bp in length 11417; cont.go of 633 bp in length

12979: gap of 13755: con'

13855: gap of

14624: co...,
1724: gap of 100 vr
15417: contig of 693 bp in teny...
15517: contig of 693 bp in teny...
18 1557: gap of 100 bp
18 15265: contig of 748 bp in length
166 15365: gap of 100 bp
17122: contig of 757 bp in length
17122: contig of 757 bp in length
17123: contig of 757 bp in length
17124: contig of 757 bp in length 33535 33634; gap of 12880 13756 14625 14725 15418 15518 19814 20588 20688 21465 21565 22332 24067 27533 8851 23201 24928 42918 8087 9714 25028 9989 22432 10484 25896 33635 Boguslawkiy, L. Boukhgalter B. Brown, D. Burkett, G. Callous, C. C Submitted (22-WAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, 1038. ON MAX 30, 2000 this sequence version replaced gi:7280305. Center: Whitehead Institute/ MIT Center for Genome Research sequencing reads that have not been assembled into contigo and in an end of a sea of separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence smpling is useful for identifying tolones to be deduced: nowers, it should not be assumed that this clone however, it should not be assumed that this clone will be sequenced to completely. In the accession number will have the while the seme that the accession number will be appeared. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green,
http://ftp.genome.washington.edu/RW/RepeatMasker.html Contact: sequence submissions@genome.wi.mit.edu 100 bp of 766 bp in length 100 bp of 761 bp in length 777 876: gap of 100 bp 101 bp yap of 100 bp 6 ... sength gap of 100 br 100 in length 100 bp f 782 bp in length 10402: gap of 100 bp 11153: contig of 751 bp in length 1153: gap of 100 bp 12005: contig of 752 bp in length 100 bp f 748 bp in length of 100 bp contig of 778 bp in length of 100 bp contig of 786 bp in length of 100 bp contig of 768 bp in length 776: contig of 776 bp in length NOTE: This record contains 122 individual Web site: http://www-seq.wi.mit.edu contig of contig of contig of contig of Center project name: L3992 Center clone name: 21\_E\_3 5927: con 6027: gap of 6788: con 3456: gap of 4204: co 7766: gap of 8552: co 9534: gap of 10302: co 6888: gap of 7666: cc 8652: gap of 9434: co 5061: 0 Center code: WIBR Direct Submission 4304: 5161: be preserved. 9535 10303 10403 11154 3357 9435 4205 6789 8553 3457

contig of 742 bp p of 100 bp contig of 774 bp

ap of 100 bp contig of 761 bp in length ap of 100 bp contig of 699 bp in length

18: gap of 142917: contig of

42218:

43017: qap of

gap of

41357

41257;

39641: 40483:

38777:

operation of 761 bp in ...
contig of 761 bp in ...
755 bp in length

atig or or occurs of 100.

to of 100 bp
st contig of 786 bp in leng.

Tig of 743 bp in length
100 bp
741 bp in length
741 bp in length

6961: contig of

61: gap of 37822: cont

37922: gap of

in length

1940: gap of 100 bp 32700: contigo of 760 bp in 2800: gap of 100 bp 33534: contigo of 734 bp in 34394: contigo of 760 bp in

contig of 757

31840:

cont.5 100 c in contig of 760 bp in 100 bp ir

gap of

34494: 35350: 36218: 37061:

35250:

50: gap of 36118: con gap of

TITLE COMMENT

100 bp in length

18950: gap of

431.98 --3300; canig or .v. -3300; gap of 100 bp 2406; contig of 766 bp in length ... < aap of '- nf 761 bp in length

24166: gap of

23300:

oof 100 bp contig of 769 bp

contig of

21564: gap of

20687:

19813:

22331;

22433

761 bp -100 bp -18 bp i

25027: gap of 25795: contig of

A 100 bp 100 bp

25895: gap of 1 26668: contig of

in length in length in length in length

743 bp 1 100 bp 1 766 bp 1 100 bp 1 769 bp 1 757 bp 1

48: gap of 1 30114: contig of 33: contig of gap of 1

29348:

0983:

31083; 31940: 32800:

.0v . 773 bp .100 bp .13 bp iv

contig of

27632; gap of 28405; con

contig of

28505: gap of 29248: con 30214: gap of

7532: contig of

gap of

26768:

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Namelial Butherial Primates; Catarrinin; Hominidae; Homo.

Manalial Butherial Primates; Catarrinin; Hominidae; Homo.

Buthovoke; J. L. Amaratunge, H. C. Are, J. R. Ayele, M. Bankar.

Batharia, J. Benton, J. Binges, K. Blankenburg, K. Bonnin, D.,

Buck, J. Benton, J. Binges, K. Blankenburg, K. Bonnin, D.,

Buck, J. Bouch, S. Brivara, M. Brown, E. Brown, M. Brynnt, N. P.

Buhay, C. Burch, P. Carter, M. Cavatos, S. R. Chacko, J. Chavez, D.

Carron, T. F. Carter, M. Cavatos, S. R. Chacko, J. Chavez, D.

Chen, G. Chen, Z. Chon, C. Crowdhy, J. Christopoules, C.

Claveland, C. D. Cox, C. Coyle, M. D. Dathorne, S. R. David, R. David, R. Dadaney, K. R. Delgado, O. Denn, A. L. Ding, Y. Dinh, H. H.

Douthwatte, K. J. Drager, H. Dugan-Rocha, S. Duthhi, K. J.

Barnhart, C. Edgar, D. Berna, A. Germer, T. Garza, M. Gill, R.

Garrell, J. M. Guevara, M. Guarathe, P. Hale, S. Hamilton, K. Harris, C. Harris, K. Harrimer, T. Garza, M. Gill, R. Gorzell, J. H. Guevara, M. Guarathe, P. Hale, S. Hamilton, K. Hennadez, O. Harris, S. Huber, J. Gorson, J. Garcis, M. Holloway, C. Holling, B. Homen, J. Jank, J. Monson, M. Hogues, M. Holloway, C. Holling, B. Homen, J. Jank, J. Monson, M. Howato, J. Moyer, S. Hume, J. Jackson, L. E. J. Li, J. J. Li, M. Louland, J. Korsh, J. Korsh, J. Karaovic, J. Li, Z. Lichaege, O. Hautis, R. Mari, M. Monson, M. Massey, B. Manhiney, E. Manhiney, E. Manhiney, E. Manhiney, E. Machen, M. Maise, M. Roll, M. Massey, B. Picker, M. Paylor, C. Shen, J. Moyer, M. Stoney, H. Mang, S. Sock, R. Parke, M. Stoney, H. Mang, S. Morte, J. Warren, M. Stoney, H. Stoney, J. Tang, H. Suthang, S. Warl, M. Stoney, H. Mang, S. Mart, M. Stoney, H. Marg, S. Mart, M. Warren, M. Warren, W. Wille, S. Mart, M. Weilling, M. Mickerson, S. Warren, R. Warling, S. Warling, A. Warren, R. Warling, S. Warling, A. Warren, R. Warling, S. Warling, S. Warling, S. Warling, A. Warren, R. Warling, S. Warling, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC078804 110ear 164456 bp DNA linear HTG 19-JUN-2002 HTG of 19-JUN-2002 ACONS SQUENCE, TY UNCAGERED FOR THE RP11-489M17, WORKING DRAFT SEQUENCE, TY uncredered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo aspiens
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                    /note="The drug associated here is was Bactrim."
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                                                                                                                                                                                                                                                                                                             Length 732;
                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                         Score 19.4; DB 6;
Pred. No. 3.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                 202
                                                                                   LEESKATIHENIGAAGFKMSP"
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                                                                                                                                                                                                                 158 9
                                                                                                                                                                                                                                                                                                                                                                                                                                   AC078804.7 GI:21431061
                                                                                                                                                                                   /replace="a"
152 c
                                                                                                                                                                                                                                                                                                             ch 92.4%;
1 Similarity 95.2%;
20; Conservative C
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Best Local Similarity
                                                                                                                          variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                 BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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LOCUS
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(Adaminam="Homo sapienn"

(Ab xref="taxon:9606"

14. 445="mink_related peptide 1, Ala substitued for Thr at
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Bikaryota, Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalia; Butheria; Primates; Catarthini; Hominidas, Homo.
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                     43886: gap of 100 bp 44672: contigo of 786 bp in length 4472; gap of 100 bp 4538: contigo of 766 bp in length 4538: contigo of 747 bp in length 4538: contigo of 747 bp in length
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55217 55928: contig of 692 bp in length
55829 56028: gap of 100 bp
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Patent: WO 0222875-A 9 21-MAR-2002;
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Location/Qualifiers
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Conservative
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Best Local Similarity
Matches 20; Conserv
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VERSION
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AUTHORS
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2. (Gasse 1 to 0'85).

S. Girler, B. L. Litton, L. Nusbeuw, C., Lander, E., Abraham, H., Allen, N., Andersen, S., Barna, N., Bastelin, V., Beda, F., Bogolalakky, L., Andersen, S., Barna, N., Bastelin, V., Gaselle, F., Golagialakky, L., Chengel, Y., Colagiel, M., Colagiel, M., Colagiel, M., Code, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Perreira, C., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Perreira, C., Coyette, M., Cage, D., Calagora, J., Gardyna, S., Gidde, S., Goyette, M., Carland, E., Carland, J., Gardyna, S., Gidde, S., Goyette, M., Linke, L., Johnson, R., Unevine, R., Heaford, A., Horton, L., Lamazaree, R., Unevine, R., Lieu, C., Liu, G., Madonald, P., Martin, N., Worben, P., Welsman, P., Welsman, C. H., O'Connor, T., Wortze, J., Welsman, C. H., O'Connor, T., O'Donnell, P., Martin, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peierre, V., Ryand, C., M., Stabeck, M., Riley, R., Schauer, S., Secery, P., Sougnes, C., Spencer, P., Santos, T., Santos, T., Santos, S., Strauss, M., Subrananian, A., Talanss, J., Wessell, R., Yiel, R., Vola, K., Kellen, M., Kill, R., Vola, K., Kellen, M., Kellen, M., Kellen, M., Kellen, M., Strauss, M., Wilson, B., M., W., Yellen, M., Kellen, M.
                                                                                                                                                                                ACO79102 64677 bp DNA linear HTG 18-AUG-2000 SAMPLINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-AUG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All respects were identified using RepeakMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
C------ Project Information
Center project name: 1,10750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             However, it should not be assumed that this clone
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-11388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This record contains 79 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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Center clone name: 113_B_8
                                                                                                                                                                                                                                                                                                                                                                               AC079102
AC079102.1 GI:9845144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                          4C079102/c
                                                                                                                                                                                                                                                                DEFINITION
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AUTHORS
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AUTHORS
                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
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NOTE: 71% is a "working draft" sequence. It currently consists of 7 contigs The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                Worley, K.C.
Direct, University
Submitted Universit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JWN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 17, 2002 this exquence version replaced gi:20335729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Assembly program: Physporer Big Dye: 24 of reads
Assembly program: Physporer Big Dye: 24 of reads
Consensus quality: 16857 bases at least Q40
Consensus quality: 16857 bases at least Q40
Consensus quality: 16890 bases at least Q30
Estimated Insert size: A53.12; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary daps between the contigg are represented as runs of N but the exect sizes of the gaps are unknown. This record will be updated with the finished sequence. This scord will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 164456;
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Location/Qualifiers
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Drafing center Code: BKD / Vewa Hogs. bcm.tmc.edu
Conteat: Ngsc.helpebom.tmc.edu
Center project manen HRPN
Center Clone name: RPI-469MT
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0; Mismatches

    164456
    organism="Homo sapiens"

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in length

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1. $6210 gap of 100 bp 12. 26524; contig of 714 bp in length 15. 72624; cancig of 714 bp in length 15. 2731; cancig of 707 bp in length 12. 28552; cancig of 701 bp in length 13. 26552; cancig of 711 bp in length 13. 26552; gap of 712 bp in length 13. 26564; concig of 712 bp in length
                                                                                                                                                                                                                                                                                              f (17)
100 bp
f 691 bp in length
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1730 bp in length
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1735 bp in length
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1723 bp in length
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1719 bp in length
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                                                                                                                                                                                                   9050. gap of 100 bp 10950. gap of 100 bp 19856. gap of 100 bp 10657; contig of 71 bp in length 10657; gap of 100 bp 11384: contig of 717 bp in length 11384: contig of 717 bp in length
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714 bp in length
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               30 bp
708 bp in length
                                              of 100 bp
contig of 724 bp in length
                                                                             of 100 bp contig of 718 bp in length
                                                                                                          of 100 bp contig of 733 bp in length of 100 bp
                                                                                                                                                           contig of 710 bp in length
of 100 bp
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                                                                                                                                                                                                                                                                                                                                      2176 12275; gap of 100 bp
2276 12981; contig of 706 bp in length
2281 13081; gap of 100 bp
3082 13796; contig of 715 bp in length
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contig of 721 bp in length
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15537: gap of
16247: contig of 710 bp in length
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contig of 735 bp in length
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contig of 738 bp in length
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22906: gap of 100 by
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             100 k
contig of 709
of
  contig
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5683: cont
15783: gap of
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6601: gap of
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8144: con
8244: gap of
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24463: con
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Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                            16073.99pc.mt.19 (100.bp)
16.1895.93c.cont.19 (102.bp)
16.1895.93c.cont.19 (102.bp)
18.1860.93c.cont.19 (103.bp)
18.1860.93c.cont.19
3611: gap of 100 bp 1435: contig of 744 bp 11 4455: gap of 100 bp 15167: contig of 712 bp 17 5567: gap of 100 bp 15577: gap of 100 bp 15577: gap of 100 bp 1777: gap of 170 bp 
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Matches 19; Conserv
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Search completed: June 9, 2003, 09:09:53 Job time : 619 secs

Probe #5189 for ge Probe #4981 used t Nucleotide sequenc Human MiRP1 homolo

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Human

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ABK86573 AAD35169 AAD35170 AAD35171

AAC64083 AAC64086 AAD35173 ABV10075 AAK74863 AAK74878

Searched:

Run on:

Database

Human genome-deriv

AAI03438 ABS03496 AAI15256

AAI04990

Probe #3597 used Probe #3429 used

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Complete genome se

AAZ01425

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AAH17956 ABL24460 ABL14198 AAI72099

2384 15987

ABL32501 ABQ67893

Human cDNA sequenc Drosophila melanog Drosophila melanog Anergy related CDN Listeria monocytog

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Human immune/haema Human immune/haema Human ovarian canc Human prostate exp

ABQ69916 AAK69409 AAK69411 ABL86737 ABV53743

ALIGNMENTS

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Chen W,

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#3482 for ge

Human Probe

40m409786

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Listeria monocytog

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Probe #14365 for gene expression analysis in human cervical cell sample.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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WO200157278-A2.
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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 Probe #14165 for g
Probe #956 used t
Puman potassium ch
Human breast cell
Human foetal liver
Probe #1463 for ge
Human brain expres
Human bone marrow
                                                                                   ; Search time 119 Seconds (without alignments) 397.411 Million cell updates/sec
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1. / S1D502/gcdata/geneseq/geneseqn-embl/NA1980.DAT:*

2. / S1D502/gcdata/geneseq/geneseqn-embl/NA1981.DAT:*

3. / S1D52/gcdata/geneseq/geneseqn-embl/NA198D.DAT:*

4. / S1D52/gcdata/geneseq/geneseqn-embl/NA198D.DAT:*

3. / S1D52/gcdata/geneseq/geneseqn-embl/NA199D.DAT:*

4. / S1D52/gcdata/geneseq
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                                                                                                                                                                                                                                                  4370478
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                          2185239 segs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            nucleic search, using sw model
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Human; Mink2; potassium channel; cardiac arrhythmia; hypertension; ds;
angina, asthma; disbetes; renal insufficiency; urinary inconfinence
in tritable colon; epilepey; cerebrowascular isofatemia; autofimmune disease.
                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at top wipo.Intr/pub/published_pet_sequences.
hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, steaging, monitoring and prognosing diseases of the human breast, particularly those diseases with polyeonic actiology. The diseases include, breast cancer, disorders of development, inflammatory diseases the breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel pocassium channel gene termed MinX2 encoding pocassium channel regulatory protein, useful for screening compounds that are useful for treating diseases caused by aberrant pocassium activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the coding sequence of human potassium channel regulatory protein, Wink2. WinX2 sequence is useful for producing a potassium channel regulatory protein useful for in vitro or in vivo screening of agonistic or antegonistic compounds that are useful for treating diseases caused by aberrant potassium activity, such as human cardiac arrhythmias, hypertension, angina, sethma, diaberes, renal insufficiency, uninary incominence, irritable colon, epilepsy, errebrance are an autonomination of tritable colon, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human potassium channel regulatory protein, Mink2, DNA sequence.
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/product= "MINK2 potassium channel protein"
                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                           Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                        non-carcinoma tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SNRP). The present sequence is one such probe. The SNRPs are detrived from human Hela celle. The SSNRPs can be used to produce a single exon microcortray, which can be used for measuring human gene expression in a sample derived from human cerrical epithelial cells. By measuring gene expression, the probes are therefore usiful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at free, wipo. Intropub/published_pot_sequences.
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                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
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Pred. No. 6.1;
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                                                                                                                                                        Claim 25; SEQ ID No 14365; 487pp; English.
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                              WPI; 2001-488901/53.
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27-SEP-2000;
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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 22; Length 450;
                             Length 450;
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2000US-0207456.
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2000US-0234687
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2000GB-0024263
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                                                                                       Conservative
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Query Match
Best Local Similarity
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03-AUG-2000;
21-SEP-2000;
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04-OCT-2000;
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                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; microarray; single exon probe; gene expression; breast;
                                                                              Score 21; DB 22; Length 372;
Pred. No. 6.1;
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                                                                                                                                                 Indela
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                             Sequence 372 BP; 110 A; 90 C; 82 G; 90 T; 0 other;
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                                                                                                                                                                                                           1 ACTITATCCAATITCACACAG 21
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2-MAY-2000; 2000US-020456.
30-JUN-2000; 2000US-068408.
21-SEP-2000; 2000US-063236.
21-SEP-2000; 2000US-023689.
                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0.
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#0200157271-A2 Homo sapiens.

ABA44797;

RESULT 4 ABA44797

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09-AUG-2001

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Gaps

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases and a a Alzaheier's disease, multiple sclerosis, soffizophrenia, epilopsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention provides a number of single exon nucleic acid
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Pred. No. 6.1;
; Mismatches 0; Indels
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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26-MAY-2000; 2000US-020756.
30-JUN-2000; 2000US-0608408.
33-AUG-2000; 2000US-063366.
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Best Local Similarity 100.
Matches 21; Conservative
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epilepsy; cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52
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03-AUG-2000;
21-SEP-2000;
                                                             Homo sapiens.
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nuclair acid probes for measuring human gene expression in a pample derived from human heart. The present sequence is one such probe. The probes may be insequence is one such probe. The probes may be insequence from the probes of predicting, measuring and displaying gene expression in semples derived from the human neart via an acroarrays By measuring gene expression, the probe are useful for predicting, disponenting gene expression, the monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                  Probe #3463 for gene expression analysin in human heart cell sample.
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                                                                                                                                                                    Human, gene expression; heart; microarray; vascular system; probe; cardòvascular disease; hypertension; cardòta arthythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 3463; 530pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-F85-2000; 200005-018912; 26-MYY-2000; 200015-0207146; 30-JIN-2000; 200015-020346; 21-S8P-2000; 200015-0244687; 27-S8P-2000; 200005-0244687; 27-S8P-2000; 200005-0244687; 27-S8P-2000; 200005-024687; 27-S8P-2000; 200005-0244687; 27-S8P-2000; 200005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-0244687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20005-024687; 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00666
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                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                            WO200157274-A2.
                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                             23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The present invention relates to human single axon nuclaic acid probes (SBNP). The present sequence is one such probe. The SBNPs are derived from human HeLa cells. The SBNPs can be used to produce a single exon microaramy, which can be used for measuring human egen expression in a sample derived from human cervical pithelial cells. By messuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical ancer. Note: The sequence data for this patent did not form pare of the printed specification, but was obtained in electronic formst directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invertion relates to single exon notlaic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placente. The probes are useful for antenatal diagnosis of human genetic disporders.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #3597 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe, microarray, human, placenta, antenatal diagnosis,
                                                                                                                                                                                                                                                                                                                        Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 21; DB 2
100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACTITATCCAATITCACACAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI34911 standard; DNA; 450 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157272-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA134911;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
        888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single evon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved dispossis and treatment of cancers such as lymphom, jetksemia and myslome. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #3482 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 21; DB 22; Length 450; 100.0%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                Example 4; SEQ ID NO: 3519; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 450 BP; 136 A; 110 C; 86 G; 118 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                            Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 ACTITATCCAATTTCACACAG 182
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                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                            Chen W,
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2000US-0234687.
2000US-0236359.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the probes of the invention.
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2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI13549 standard; DNA; 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                            Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488901/53
                                                                                                                                                                                                                                    WPI; 2001-488900/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157278-A2.
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                            Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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(first entry)

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The invention relates to a spatially-addressable set of single exon nucleic and probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes for measuring gene expression in a sample derived from the 1254 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 1254 open reading frames derived from the 1254 or probes. He novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with complement of detectably babeled mucleic acid derived from human lung comprising (a) contacting the array with complement of detectably bedied mucleic acid derived from human lung comprising (a) algorithmically predicting at least one exon from genemic sequences (c) the euksyote; and (b) detecting specific phyridisation of detectably labeled mucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon from genemic sequences (c) the euksyote; and (b) detecting specific phyridisation of detectably labeled mucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon probe of the exons and (b) measuring the expression of each of the exons in several correcting the expression of the exons in the tissues and/or cell types with the exon, where a common pattern of microarray having a probe with the exon, where a common pattern of the exons should be assigned to a single exon probes of the exons and the tissues and/or cell types with the exons where a common pattern of the exons and the exons in the tissues and/or cell types indicting the expression of each of the exons and the exons and
                                                                                                                                                Human; de; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstital lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; Hermann-Pick disease; Hermann-Pick disease; Hermann-Pick disease; Hermann-Pick disease; Pulmonary, Parlocine; Syndrome; astrocidosis; pulmonary placediserosis; pulmonary placediserosis; pulmonary placediserosis; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary hymogenis; karagener syndrome; pulmonary dysplasia; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                         Human genome-derived single exon probe from lung SEQ ID No 3487.
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ABS03496 standard; DNA; 450
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                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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03-AUG-2000;
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27-SEP-2000;
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                                        ABS03496;
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The present invention relates to movel unique exon mucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast smaple, where the probe hybridises at high stringency to a nuclinic acid expressed in the human breast. The probes are useful for predicting disgnosing grading stripping the probes are useful for predicting disgnosing grading stripping disnesses of the human present particularly showed these are with polygonic acid property of the human present cancer, disorders of descripent, inflammatory diseases of the breast cancer, disorders of descripent, inflammatory diseases of the breast cancer disorders.
                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                           Probe #3429 used to measure gene expression in human breast sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                        162 ACTITATCCAATITCACACAG 182
                    ACTITATCCAATITICACACAG
                                                                                                                                                                 AAI03438 standard; DNA; 450 BP
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2000US-0632366.
2000US-0234687.
2000US-0236359.
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Matches 21; Conservative
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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Chen W, Rank DR,

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2000US-180312P. 2000US-207456P. 2000US-0608408. 2000US-234687P. 2000US-236359P. 2000GB-0024263

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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe are useful for messuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting a dispression in the human breast, monitoring and proquesting diseases of the human breast, particularly those diseases with polygenic actology. The diseases include a breast cancer, disorders of descoperur, inflammentory diseases of the breast cancer, disorders of descoperur, inflammentory diseases of the breast cancer, disorders of descoperur, inflammentory diseases of the breast cancer of descape and accompany.
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                                                                                                      DB 22; Length 471;
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                                                         Sequence 471 BP; 148 A; 102 C; 86 G; 135 T; 0 other;
                                                                                               100.0%; Score 21; DB 2
100.0%; Pred. No. 6.1;
            at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                  0; Mismatches
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                                                                                                                            1 Similarity 100.0%;
21; Conservative 0
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
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03-AUG-2000;
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(CODD), interstitial lung disease (ILD), familial idiopathic pulmonary fibroes, neurofibroatesis, tuberous soletesis, doubler's disease. Namenani Pickersis, doubler's disease. Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hall sticoyrosis. Jumphangiolisionyconocisis, pulmonary diveolar proteinosis, Karagener syndrome, fibrocoystic pulmonary diveolar proteinosis, Karagener syndrome, fibrocoystic pulmonary dysplass, primary offistingsis, pulmonary hypertension probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fibromary displayment directly from WIPO at
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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21-SEP-2000;
27-SEP-2000;
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gastric acid secretion, anti-arrhythmic agent; myocardial infarction; ss.
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Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of human potassium channel subunit IsK2.
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/product= "potassium channel subunit IsK2"
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79..450
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                                                                                                                                                                                    AAF80269 standard; DNA; 471 BP
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tes 21, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                            29-JUN-2001
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                                                                                                                                 RESULT 15
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Search completed: June 9, 2003, 08:51:24 Job time : 121 secs

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9, 2003, 08:36:51; Search time 31.5 Seconds (Without alignmente) 204,451 Million cell updates/sec
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2: /cgm2 6/pcodata/l/ina/se_CONB seq:*
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4: /cgm2 6/pcodata/l/ina/se_CONB seq:*
5: /cgm2 6/pcodata/l/ina/se_CONB seq:*
6: /cgm2 6/pcodata/l/ina/backfilesl seq:*
6: /cgm2 6/pcodata/l/ina/backfilesl seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TRIERATION TOR SED 1D NO. 36: SEQUENCE CHARACTERISTICS: LENGTH: 640 base pairs TYES: nucleic acid STRANDSNESS: adulte TYES: nucleic TYES: not relevant NOLECULE TYES: OBLIERATION: NO CHICINAL SOURCE: ORGANISM: PLG

303/499-8080

TELEPHONE:

10.56 in US-08-121-202-1 10.70 in US-08-121-202-1 10.70 in US-08-6-08-131-1 10.70 in US-08-212-137A-1 10.70 in US-08-212-137A-1 10.70 in US-08-170-12-1 10.70 in US-08-170-12-12-12-12-12-12-12-12-12-12-12-12-12-	GENERAL IN OGRAFION: GENERAL IN OGRAFION: APPLICANT MCDILAY, John S. TYLIE OF INDEMITION: Hybrid Human// NUMBER OF SEQUENCES: CORRESPONDED: ADDRESS: CORRESPONDED: ADDRESS: CORRESPONDED: ADDRESS: CONFUTER: Boilder CITY: Boilder CITY: Boilder COUNTRY: USA COMPUTER: READALE FORM: MEDIUM TYPE: IDH PC COMPALIANE COMPUTER: THE PC COMPALIANE COMPUTER: THE PC COMPALIANE COMPUTER: THE PC COMPALIANE COMPUTER: THE STATE: ADDRESS: COMPUTER: THE STATE: APPLICATION NATA: APPLICATION NUMBER: US/08/670, THE APPLICATION NUMBER: WO PCT/US94, RILING DATE: 15-40V-1994 PRICE THING DATE: 11-40V-1994	winner a n Circle isk bookmarble arible skob/ms-D 10ase #11 skob/670 996 0 PCT/US 994	STREET: 5310 Manhattan Circle CITY: Boulder COLOCAGO COUNTRY: COLOCAGO COUNTRY: USA MEDIUN TYEE: FORDER COMPUTER READALE FORM: COMPUTER: IMP PC COMPALIBLE COMPUTER: IMP PC COMPALIBLE COMPUTER: PC-LOS/NS-DOFENTARE: DC-LOS/NS-DOFENTARE: DC-LO
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                                                                                                                                                                                                                                                                                                                                                                             TILE BERENGE (1 ) 5-93.

CURRENT PELICATION NUMBER: US/09/315,179
CURRENT PELICATION NUMBER: US. 09/037,601
EARLIER PELICATION NUMBER: US. 09/037,601
EARLIER FILING ADER: 1996-03-10
EARLIER FILING ADER: 1996-03-10
EARLIER FILING ADER: 1997-06-28
EARLIER FILING ADER: 1997-07-10.
EARLIER FILING ADER: 1997-07-10.
EARLIER FILING ADER: 1997-07-10.
EARLIER FILING ADER: 1997-07-10.
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TIPLE ON INVENT M. MODIFIED FACTOR VIII
FILE REFERENCE: 75 55 100 MERCA.
CURRENT FILING NEWS. 105/03/525 656
CURRENT FILING NEWS. 200/03/001
EARLIER FILICATION WINERS. 03/03/601
EARLIER FILICATION WINERS. 03/03/00
EARLIER FILICATION WINERS. 03/03/00
EARLIER FILICATION WINERS. 03/03/00
EARLIER FILING DAIR: 1996-06-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FALCHIN VET. 2.0
SEQ ID NO 29
LEMOTH: 6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.4;
Pred. No. 40
                                                                                                                                                                                                                                                                                            APPLICANT: Lollar, John S
TITLE OF INVENTION: Modified Factor VIII
FILE REFERENCE: 75-95H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09523656; Patent No. 6458563; GENERAL INFORMATION:
                                                                                                                                                                                        Sequence 36, Application US/09315179
Patent No. 6376463
         3116 TTTATCCAATTTGACACA 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3116 TTTATCCAATTTGACACA 3099
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(6399)
US-09-315-179-36
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                  RESULT 3
US-09-315-179-36/c
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US-09-523-656-29/c
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                                                                                                                              Omery Match 78.1%; Score 16.4; DB 2; Length 6402; Best Local Similarity 94.4%; Pred. No. 40; Marches 17; Conservative 0; Manaches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vegenare 3.6. Application US/09037601
Patent No. 6180371
GENERAL INFORMATION:
APPLICANT 10.1187. John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
CORRESPONDENCE ADDRESS: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Greenlee, Winner and Sullivan, P.C. CTREETS 5370 Manhattan Circle Suite 201
CTTY: Boulder
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.1%; Score 16.4, Dl
Best Local Similarity 94.4%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: 75-
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
TOPOLOGY: not relevant
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
, NAME/KEY:
, LOCATION:
US-08-670-707A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -09-037-601-36/c
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Gaps

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US-09-147-522-5

Sequence 5. Application US/09147522

Sequence 5. Application US/09147522

SEQUENCE 5. Application US/09147522

SEQUENCE 5. Application US/09147522

SEQUENCE 5. Application SIMONA

APPLICANT: BENATI, LUCA

APPLICANT: SECLALCANT: CARRELA

APPLICANT: SPCIALCANT: CARRELA

APPLICANT: SPCIALCANT: CARRELA

APPLICANT: SPCIALCANT: CARRELA

APPLICANT: CONTINGENT US/05

TITLE OF INVENTION: PROCESS FOR ITS FREPARATION

TITLE OF INVENTION: PROCESS FOR ITS FREPARATION

CURRENT APPLICATION WINNERS: 1059-01.14

SEALLIER APPLICATION WINNERS: 1997-07-03

SCOTTMARE: PARELING DATE: 1997-07-03

SCOTTMARE: PARELING USC: 9.0

SCOTTMARE: PARELING USC: 9.0

LENGTH: 500

LENGTH: 500
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| Sequence 1. Application US/08203532F
| Sequence 1. Application US/08203532F
| Setting 1. Application US/08203532F
| Setting 1. Application US/0820353F
| ApplicANT: Gorski, David H. ApplicANT: Gorski, David H. ApplicANT: Gorski, David H. TITLE OF INVENTION: Growth Arrest Homeobox Gene UNMERS OF SEQUENCE: 19
| COMPRES: Objection Office Halter, and Griswold STREE: Objection Avenue COMPRES: Objection Avenue STRIE: Objection Avenue STRIE: Objection Avenue COMPRES: Discourate Halton Avenue COMPUTE: INFO Compatible COMPUTE: REALDALE FORM: PC-DOS/MS-DOS SOFTWARE: Retentin Release #1.0, Version #1.25 APPLICATION WIMMED: US-ACCORDATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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FILING DATE.
CLASSPECATION: 435
ATTORNEY, FAGATT INFORMATION:
NAME: GOLITCK, Mary E.
REGISTRATION NUMBER: 44829
REFERENCE/DOCKET NUMBER: 22311/00114
TELECOMPUTICATION INPORMATION:
TELECOMPUTICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2587 ACTITATICAATITCAGAC 2605
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INFORMATION FOR SEQ ID NO: 58QUENCE CHARACTERISTICS: LENGTH: 2244 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (216) 241-0816
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: CDS
; LOCATION: (47)..(1507)
US-09-147-522-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Sequence 25, Application US/09198603C
Sequence 25, Application US/09198603C
Remain No. 201139
Remain No. 201103
Remain N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 627;
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                                                            1; Indels
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Pred. No. 57;
0; Mismatches
      Best Local Similarity 94.4%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                          3116 TTTATCCAATTTGACACA 3099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TITATCCAATTICACACAG 21
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                                                                                                                                                3 TITATCCAATTICACACA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
, LOCATION: (1)..(627)
US-08-962-281-1
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Matches 17; Conserv
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US-09-198-603C-25
                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-962-281-1/c
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LENGTH: 1211
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LENGTH: 627
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RESULT 7

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CORRESPONDENCE ADDRESS:
ADDRESSES: Calfee, Halter, and Griswold STREET: 800 Superior Avenue CITY: Cleveland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22311/00114
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ATTORNEY/AGENT INFORMATION:
NAME: GOLIGA, MARY E. REGISTRATION NUMBER: 3-48.
REGISTRATION NUMBER: 2233
REFERENCE/DOCKET NUMBER: 2233
TELECHANDICATION:
TELECHA
                                                                                         1314 ACTITCICCAATITCAC 1298
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2244 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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LOCATION:
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US-08-845-258-3
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ZDP: 4414-268 PRW:
COMPUTER READABLE FORM:
MEDIUN TYPE: IDOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC COMPACIBLE
SOFWARE: PATENTIN RELEASE #1.0, Version #1.25
MPPLICATION NUMBER: US/09/078,465
FILING DATE: 44-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sequence 1, Application US/09078465 | Patent No. 280969 | Patent No. 280969 | GENERAL INVORMATION: APPLICANT: Gorski, David H. APPLICANT: Malsh, Kenneth F. TITLE OF INVENTION: Growth Arrest Homeobox General Correspondences: 19 | CORRESPONDENCES: 10 | CORRESPONDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/203,532
FILING DATE: 24-FEB-1994
ATORREY LAGRAT INFORMATION:
NAME: GOLICAC, MARY E:
REGISTATION NUMBER: 348.99
REFERENCE DOCKET NUMBER: 2311/00114
TELECOMMUNICATION INFORMATION:
TELEFONE (25:0) 241-0816
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                  LOCATION: 197.1108
US-08-203-532F-1
STRANDEDNESS: both
                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                          HYPOTHETICAL: NC
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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Gaps
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Fatent No. 618396
GENERAL INFORMATION:
APPLICANT: Reed, Even G.
APPLICANT: Lodges, Michael J.
APPLICANT: HOUGHOUT, RAYMOND
APPLICANT: Glasth, Paul R.
ITILE OF INVERTION: COMPOUNDS AND WETHODS FOR THE DIAGNOSIS
TITLE OF INVERTION: AND TREATMENT OF B. MICROTI INPECTION
WORNER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                        ZIF: 44114-7689
COMPUTER REAGABLE FORM:
MEDIUM TYPE: FLOPDy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: THE PC COMPALIBLE
COMPUTER: FOLDS/MS-DOS
SOFTWARE: PATENTIAL Release #1.0, Version #1.25
SOFTWARE: PATENTIAL NAME:
APPLICATION NUMBER: PCT/US95/01882A
FILING DATE:
PCT-1959-101892A-1/C
SQUENCE 1 APPLICATION PC/TUS9501882A
GRNERAL INFORMATION:
APPLICANT: GOASE, David H.
APPLICANT: GOASE, David H.
APPLICANT: Walsh, Kenneth
APPLICANT: Walsh, Kenneth
APPLICANT: Walsh, Kenneth
APPLICANT: Walsh, Kenneth
NUMBER OF SUFORMERS: 4
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Patent No. 618376
GENERAL INFORMATION:
APPLICANT: Reed, Stewn G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Reymond
APPLICANT: Sleath, Paul R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
ITILE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
CORRESSED. SUBJECTS:
ADDRESSEE SEEN, AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2430;
                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floopy disk.

COMPUTER: INY FC. COMPUTISH:

SOFTWARE: PARCETIN FORMER:

CUMRENT APPLICATION NOMER: US/08/45,258

FILLING DATE: 24.4AP-1997

ATTORNEY/AGENT INFORMATION:

MARE: MARI, DATA 13-5

REGISTRATION NUMBER: 31,392

REFERENCE/OCKET NUMBER: 31,392

REFERENCE/OCKET NUMBER: 31,392

TELECONMUNICATION INFORMATION:

SEQUENCE: (206.682-603)

INFORMATION FOR SEC ID NO: 3:

SEQUENCE: CANASACTERISTICS:

"WATH. 3430 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.3%; Score 15.4; DB 4; Best Local Similarity 94.1%; Pred. No. 1.1e+02; Macches 16; Conservative 0; Mismatches 1.
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NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/845,259
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTATCCAATTTCACACA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
                                                 CITY: Seattle
STATE: Washington
                                                                                                             USA
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                                                                                                         COUNTRY:
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Sequence 1, Application US/08990571
Patent No. 6214377
EGNRAL INFORMATION:
CRARAL INFORMATION:
TITLE OF INVESTIGATION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M. NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS: SED AND BERRY
STREET: 6300 COlumbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-990-571-40/c
; Sequence 40, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G. et al.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
                                                                                                                                                                                                                             ö
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WEDING TYPE: Ploppy disk
COMPUTER: IES POPPY disk
COMPUTER: IES POPPY disk
SOFTWARE: STSTEM: CC.TDGS/MS-DGS
SOFTWARE: POPPY Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/990,571
FILMS DATE: 1-DEC-1997
                                                                                                                                                                                     73.3%; Score 15.4; DB 4; I 94.1%; Pred. No. 1.1e+02; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%; Score 15.4; DB 4;
94.1%; Pred. No. 1.1e+02;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MAKE, DAVId J.
ROATSTRATTON NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
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INPORATION FOR ESQ ID NO: 3:
SEQUENCE CHARACTRISTICS:
LENCAT: 2430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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(206) 622-4900
                                                                       LENGTH: 2430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 94.1:
Matches 16; Conservative
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nes 16, Conservative
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Washington
                                                                                                                              linear
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US-08-990-571-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washir
COUNTRY: USA
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                                                                                                                              ; TOPOLOGY:
US-08-845-258-40
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TELECOMMUNICATION INFORMATION

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APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
APPLICANT: GORDENCES: 49
CORRESPONDENCES. AND TREATMENT OF B. MICROTI INFECTION
NUMBES OF SEQUENCES: 49
ADDESSERS: GED AND BERRY
ADDESSERS: GED AND BERRY
CORPUTER: GOOD COLUMBIA Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
CITY: Seattle
CITY: Seattle
CITY: Seattle
COMPUTER: RADBAILE FORM:
COMPUTER: IBM FO COMPATIBLE
COMPATING SYSTEM: FOLDOS/MS-DOS
SOFTMARE: Patentin Release #11.0, Version #1.30
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73.3%; Score 15.4; DB 4; Length 2430;
Best Local Similarity 94.1%; Pred No. 1.1e-02;
Matches 16; Conservative 0; Mismaches 1; Indels 0;
Matches 16; Conservative 0; Mismaches 1; Indels 0;
                                                                                                                                                                                                    COMPUTER READALS FORM:
MEDION TYPE: Ploppy disk
MEDION TYPE: Ploppy disk
OCMPUTER: 138 PC Compatible
OFFAKTING SYSTEM: PC-DOS/MS-DOS
OFFAKTING SYSTEM: PC-DOS/MS-DOS
OFFAKTING SYSTEM: Release #1.0, Version #1.30
CURRENT APPL/CATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION UNDER: US-0.1997
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
STED AND BERRY
STREEF: 6500 COlumbia Center, 701 Fifth Avenue
CITY: Seartle
STATE: wathington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Warth d.
REGISTRATION NUBER: 31,392
REPERENCE/DOCKET WINBER: 210121.426C3
TELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECHAX: (206,662-603)
INFORMATION FOR EQU ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 2430 base pairs
TYPE: Mulleic acid
STRANDEDMESS: single
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REFERENCE/DOCKET NUMBER: 210121.426
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FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONNEY,AGENT HORDWATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08723142A
Patent No. 6306396
GENERAL INFORMATION:
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| TELEPHONE: (706) 522-4900 | TELEPHONE: (706) 522-4900 | TELEPHONE: (706) 522-4900 | TELEPHONE: (706) 622-4900 |
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9, 2003, 09:12:21 ; Search time 59.5 Seconds (Without alignmenta) 493.594 Willion cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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21
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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Pred. No. is the number of results predicted by chance to have a corce greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 33139, A	Sequence 3463, Ap	Sequence 16671, A	Sequence 5, Appli	Sequence 1, Appli		Sequence 9715, Ap	Sequence 31400, A	Sequence 22, Appl	Sequence 2479, Ap	Sequence 36, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 7825, Ap	Sequence 530, App	Sequence 105, App	Sequence 409, App	Sequence 1010, Ap	Sequence 13864, A	
SUMMARIES	ΩI	US-09-864-761-33139	US-09-864-761-3463	US-09-864-761-16671	US-10-000-151B-5	US-10-227-195A-1	US-10-227-195A-2	US-09-867-701-9715	US-09-918-995-31400	US-09-776-724A-22	US-10-198-846-2479	US-10-187-319-36	US-09-949-654-3	US-10-329-960-1	US-09-918-995-7825	US-09-969-708-530	US-10-091-438-105	US-09-764-853-409	US-09-764-877-1010	US-10-198-846-13864	
	DB	10	10	10	σ	σ	σ	10	σ	σ	đ	Ø	10	σ	σ	10	6	10	10	6	
	Match Length DB ID	372	450	471	732	113604	113604	339	461	752	893	6402	368004	1830121	431	870	1273	1273	1273	1825	
	Match	100.0	100.0	100.0	100.0	100.01	100.0	78.1	78.1	78.1	78.1	78.1	78.1	78.1	77.1	77.1	77.1	77.1	77.1	77.1	
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Sequence 2266, Ap Sequence 2026, Ap Sequence 2008, Ap Sequence 76, Appliserunce 111, Appliserunce 111, Appliserunce 111, Appliserunce 118, Appliserunce 180, Appliserunce 180, Appliserunce 209, Appliserunce 209, Appliserunce 209, Appliserunce 209, Appliserunce 209, Appliserunce 200,
10 US 09 980-107-2268 10 US-10-980-107-2268 10 US-10-980-107-208
4656 10101 11488 11488 41160 14160 1
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0.0 0.0 0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0

RESULT 1

ALIGNMENTS

ACID PROBES USEFUL FOR

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0.00-864-761-33139 ; Sequence 33139, Application US/09864761 ; Patent No. US2002048763A1 ; GENERAL INFORMATION:	; APPLICANT: Penn, Sharron G. ; APPLICANT: Rank, David R.	Hanzel, Davi	; APPLICANT: Chen, Wensheng · TITLE OF INVENTION: HIMAN GENOME-DERIVED SINGLE EXON MICHEL	OF INVENTION: GENE EXPRESSION ANALYSIS BY	FERENCE: Aeomica-X-1	APPLICATION NU	<pre>; CURRENT FILING DATE: 2001-05-23 ; PRIOR APPLICATION NUMBER; US 60/180.312</pre>	FILING DATE: 2000-02-04	APPLICATION N	FILING DATE: 2000-05-26	APPLICATION N	FILING DATE: 2000-08-03	; PRIOR AFFILCATION NUMBER: GB 24263.6	APPLICATION N	FILING DATE: 2000-09-27	APPLICATION N	FILING DATE: 2001-01	APPLICATION N	FILING DATE: 2001-01	APPLICATION N	FILING DATE: 2001-01	. PRIOR AFFILIATION NUMBER: PCI/USUI/U0669	APPLICATION N	FILING DATE: 2001-01	APPLICATION N	FILING DATE: 2001-01	APPLICATION N	; PRIOR FILING DATE: 2001-01-30	PILING DATE: 2001-01	APPLICATION N	
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                                                           HRIOR APPLICATION NUMBER: PCT/USO1/00670
HRIOR APLINGTHAND: UNDOS. U.S. 60/234,687
HRIOR APLINGTHAND: USO 60/234,687
HRIOR PELINGTHAND: USO 60/234,687
HRIOR PELINGTHAND: USO 60/20 60/20
HRIOR PELINGTHAND NUMBER: US 09/608,408
HRIOR PELINGTHAND NUMBER: US 09/774,203
HRIOR PELINGTHAND NU
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                         FILING DATE: 2001-01-30
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: MICK, David K.
APPLICANT: HAREL, David K.
APPLICANT: HAREL, David K.
APPLICANT: Chen, Wensheep TITLE OF INVENTION: HUMAN GENOME-DERIVED GINGLE EXON NUCLEIC ACID PROBES USBFUL FOR TITLE OF INVENTION: GENE EXPRESSION AMALYSIS BY MICKOARRAY
FILE REPERBUCE: Aconica-K.
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OTHER INFORMATION: EXPRESSED IN HELLOO, BIGNAL = 0.67
OTHER INFORMATION: EST HIMPAN HIT: A.165452.1, EVALUE 0.00e+00
OTHER INFORMATION: SEX.EMPEN HIT: 097656, EVALUE 0.00e-67
OTHER INFORMATION: WITHIT: 9111526220, EVALUE 0.00e+00
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100.0%; Pred. No. 3.2;
tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FLILING MADAFE: 2001-01-30
PRIOR FLILING MADAFE: 2000-00-31
PRIOR PLILING MADAFE: 2000-00-30
PRIOR FLILING MADER: US 09/608,408
PRIOR FLILING MADER: US 09/608,408
PRIOR FLILING MADE: 2000-06-30
PRIOR PLILING MADE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117,203
SOFTHARE: ANDOWN SEQUENCE Listing Engine vers: 1.1
SOFTHARE: ANDOWN SEQUENCE Listing Engine vers: 1.1
SOFTHARE: 372
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CURRENT PELICATION NUMBER: US/09/864,761
CURRENT PELICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-20
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR FILING DATE: 2000-06-30
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR PELICATION NUMBER: US/09/32,366
PRIOR PELICATION NUMBER: US/09/32,369
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
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PEATURE INFORMATION: MAP TO OTHER INFORMATION: EXPREOTHER INFORMATION
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 21; Conserv
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Farent No. USCOUZO132237A1
GENERAL INCOMPATION
FAPLICANT HAJACE Paul A.
APPLICANT HAJACKET SHAIL L.
TITLE OF INVENTION: CANDOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: CANDOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: CANDOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TOTALENT PELLICATION NUMBER: US/09/667,701
CURRENT PELLICANION NUMBER: US/09/667,701
NUMBER OF SEG ID NOS: 10912
SOFTWARE: FESTEEQ for Windows Version 4.0
SEQ ID NO 9715
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 9; Length 113604; 100.0%; Pred. No. 8.8;
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APPLICANT: Arnoid, Dean
APPLICANT: Arnoid, Dean
TITLE CHERENCE: 1030U1
CURRENT PELLOR DATE: 20301.10-18
CURRENT PELLOR DATE: 2002-11-18
WHORES OF SEQ 1D NOS: 2
SOFTWARE: PSESSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                  NAME/KEY: misc_feature; NAME/KEY: misc_feature; LOCATION: 175, 7204, 36973, 66372, 76921, 81512, 88727 US-10-227-1595A-1
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        CURRENT APPLICATION NUMBER: US/10/227,195A
CURRENT FILING DATE: 2002-11-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-867-701-9715
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Matches 21; Conserv
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                                                                                                                                                           ORGANISM: Human
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                                                                                              SEQ ID NO 1
LENGTH: 113604
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LENGTH: 113604
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| Publication No UGZ0010077633A1
| Publication No UGZ0010077633A1
| APPLICANT Cox, David APPLICANT Armold, Dema | TITE OF INTENTION: Haplotype structure of chromosome 21 | FILE REFERENCE: 103001
OTHER INFORMATION: MAP TO APONO120.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELAO, SIGNAL = 0.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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// Publication No. US20030013136A1
// GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Matches 21, Conserva
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Sequence 2799, Application US/10198846
| Sequence 2799, Application US/10198846
| Publication No. US20030059974A1
| SERNEAL INFORMATION:
| APPLICANT: Lilia, James
| APPLICANT: Lilia, James
| APPLICANT: Steinmann, Kathleen
| TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
| TITLE OF INVENTION: POR IDENTIFICATION ASSESSMENT, PREVENTION, AND
| TITLE OF INVENTION: THEREPROSES METHODS OF INVENTION: THEREPREVENTION HOMBER: US/10/198, 846
| CURRENT APPLICATION NUMBER: US/10/198, 846
| CURRENT FILIAND DITE: 2002-07-18
| FRIOR PELIAND DITE: 2003-07-18
| FRIOR PELIAND DITE: 2003-07-18
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742,
825,
873,
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SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 2479
LENGTH: 893
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726,
820,
866,
                PRIOR PRING DATE. 1997-07-16
PRIOR APPLICATION WANGER, 60/05.)440
PRIOR APPLICATION WANGER, 60/05.)440
PRIOR APPLICATION WANGER, 60/05.)441
PRIOR APPLICATION WANGER, 60/05.)441
PRIOR PRIOR THING DATE. 1997-07-22
PRIOR PRIOR THING DATE. 1997-08-18
PRIOR PRIOR THING DATE. 1997-08-18
PRIOR PLICATION WANGER, 60/055, 985
PRIOR PLICATION WANGER, 60/055, 946
PRIOR PLICATION WANGER, 60/055, 946
PRIOR PLICATION WANGER, 60/055, 946
PRIOR PLICATION WANGER, 1997-08-18
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Best Local Similarity 94.44
Matches 17; Conservative
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ORGANISM: Homo sapiens
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LOCATION: 808, 8
LOCATION: 846, 8
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94.4%; Pred. No. 3.76+02; ... wigmatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HyseG Inc.
THOSE OF INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LINRARIES
FILE REPRENCE. 2041.7-75
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 1099-01.07-07-30
PRIOR APPLICATION NUMBER: US/09/215,076
PRIOR PELING PATE: 1999-01.20
NUMBER OF SEQ ID NOS: 38054
SOUTHARE: PARESEQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INTOGRATION 64 Human Secreted Proteins TITLE OF INVESTIONS 64 Human Secreted Proteins FILE REPRENCE: PZ011

CURRENT PEDICATION NUMBER: US/09/776.724A

CURRENT FILING DATE: 2001-02-06

PRIOR PELICATION NUMBER: 09/669,688

PRIOR PELICATION NUMBER: 09/669,688

PRIOR PELICATION NUMBER: 09/69,982

PRIOR PELICATION NUMBER: 09/69,688

PRIOR PELICATION NUMBER: 09/69,618

PRIOR PELICATION NUMBER: 60/052,661

PRIOR PELICATION NUMBER: 60/052,818

PRIOR PELICATION NUMBER: 60/052,819

PRIOR PELICATION NUMBER: 60/052,819

PRIOR PELICATION NUMBER: 60/052,819

PRIOR PELICATION NUMBER: 60/052,819

PRIOR PELICATION NUMBER: 60/052,819
                                                                                                                                                                                                                                                                                                                       Sequence 31400, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1)...(461)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                         160 ACTITITICCAATITICACA 177
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                                                                                                                 1 ACTITATCCAATITCACA 18
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                        Best Local Similarity 94.49
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 461
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CHERAL INCOMATION: CONTROL OF THE MEMORY ON THE MEMORY OF 
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Sequence 3. Application US/09949654

Sequence 3. Application US/09949654

GENERAL INCERATION.

APPLICATI YAN, Chunhua et al.

APPLICATI YAN, Chunhua et al.

TITLE OF INVENTION: INCLED ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: ADMINISTRATION: ACID ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: LOOP 12.

CHERENT APPLICATION WHORER: US/09/949,654

CURRENT FILING DATE: 2001-09-12.

PRIOR PALLOR APPLICATION WHORE: 60/211,572

PRIOR FILING DATE: 2003-09-11.
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78.1%; Score 16.4; DB 10;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Marchee 17; Conservative 0; Mismatches 1;
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SOFTWARE: PastSEQ for Windows Version 4.0
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LOCATION: (9921)..(9921)
OTHER INFORMATION: n equals a, t, g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(368004)
CTHER INFORMATION: n = A,T,C or G
US-09-949-654-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-329-960-1; Sequence 1, Application US/10329960; Publication No. US20030099277A1
3116 TTTATCCAATTTGACACA 3099
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OTHER INFORMATION: n equals a,
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LOCATION: (10150)..(10150)
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LOCATION: (4747)..(4747
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ORGANISM: Human
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                                                                                                 Ouery Match 78.1%; Score 16.4; DB 9; Length 893; Best Local Similarity 94.4%; Pred. No. 4.44e-07. And Matches 17; Conservative 0; Mismatches 17; Indels Matches 17; Conservative 0; Mismatches 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
CORRESPONDER ADDRESS:
CORRESPONDER ADDRESS:
STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYETEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION WHORE: US/10/187,319
FILING DATE: 27-ANG-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Greenlee, Lorance L. REGISTRATION NUMBER: 27,894
REFERENCE/DOCKET NUMBER: 75-95K
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ 1D NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 36, Application US/10187319
; Publication No. US20030068785A1
; GENERAL INFORMATION;
i OTHER INFORMATION: n = A, T, C or G
US-10-198-846-2479
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TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 36:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                      576 TTAACCAATTTCACACAG 559
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MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                        4 TTATCCAATTTCACACAG 21
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COMPUTER READABLE FORM:
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Best Local Similarity 94.44
Matches 17; Conservative
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ORIGINAL SOURCE:
ORGANISM: Pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-187-319-36/c
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; FEATURE: ; NAME/KEY: ; LOCATION: (80024) ; OTHER INFORMATION: n equals a, t, g or c	; FABLUKE: NAME/KEY: misc feature ; IOCATION: (100091)(100091) ; OTHER INFORMATION: n equals a, t, g or c.	NAMP/KEY: misc feature LOCATION: (102596)(102696) O'THER INFORMATION: n equals a, t, g or c	) FALUNE: ) NAMP/KRY: misc feature ) LOCATION: (105121)(105121) ) OTHER INFORMATION: n equals a, t, g or c PEATURE:	NAME/KEY: misc_feature ; LOCATION: (107248). (107248) ; OTHER INFORMATION: n equals a, t, g or c ; FEATURE.	NAME/KEY: misc reacure LOCATION: (117136) OTHER INFORMATION: n equals a, t, g or c FEATURE:	, NAME/KEY: MREC IERUIPE ; LOCATION: (119750) . (119750) ; OTHER INFORMATION: n equals a, t, g or c ; FEATURE:	) NAME/KEY: misc feature ; LOCATION: (119924)(119924) ; OTHER INFORMATION: n equals a, t, g or c ; FEATURE:	NAME/KEY: misc_feature; ; LOCATION: (120038). (120038) ; OTHER INFORMATION: n equals a, t, g or c; ; FEATURE:	NAME/KEY: misc feature LOCATION: (121344). (121344) OTHER INFORMATION: n equals a, t, g or c PEATURE:	NAME/KEY: misc feature 1.COATION: (122167) . (122167) OTHER INFORMATION: n equals a, t, g or c FEATURE:	NAME/KEX: misc feature   LOCATION: (122336)(122336)   OTHER INFORMATION: n equals a, t, g or c   FEATURE:	) NAME/KAS: NASC _EGALUS ) OTHER INFORMATION: n equals a, t, g or c ) FEBTURE: NAME/CVV. misc feature	CCATION: (131360); (131360); OTHER INFORMATION: n equals a, t, g or c FEATURE:	NAME/KEY: misc feature LOCATION: (139910) . (139910) OTHER INFORMATION: n equals a, t, g or c FEATURE:	NAME/KRY: misc_feature LOCATION: (140398) . (140398) OTHER INFORMATION: n equals a, t, g or c FEATURE:	NAMENGARIAN MARC LEGALISA LOCATION: (142750)(142750) OTHER INFORMATION: n equals a, t, g or c FRETURE:	APPLACATION: (145058). COTHER INFORMATION: n equals a, t, g or c ; FRATURE:
t, g or	OTHEK INCOMMATION: n equals a, t, g or c NAME/KEY: misc feature LOCATION: (36543). (36543)	j .	Other incommittion in equals a, t, g or c FEATURE: NAME/KEY: misc feature LOCATION: (36556). (36536) OTHER INCOMMITTOR: n emnis a. t. q or c	t, 9 or	PEATURE: NAME/INST. misc_feature LOCATION: (44416). OTHER INFORMATION: n equals a, t, g or c	FRATURE TEATURE TO THE SECOND TO THE SECOND TO THE SECOND THE SECO	PEATURE PEATURE TO PEATURE LOCATION: (44975). (44975) OTHER INFORMATION: n. equals a, t, g or c	į,	PEATURE NAME/KEY: misc_feature LOCATION: (45732). OTHER INVORVATION: n equals a, t, g or c	; Y: misc_feature N: (47036)(47036) NFORMATION: n equals a, t,	: Y: misc_feature N: (51334)(51334) NFORMATION: n equals a, t,	FEAUNGY. NAMA/KET: misc feature LOCATION: (51602)(51602) OTHER INFORMATION: n equals a, t, g or c	NAME/KEY: misc_feature LOCATION: (\$1786) OTHER INPORANTION: in qualle a, t, g or c	PRATURE NAME/KRY: misc_feature LOCATION: (\$1869: 1.61805) OTHER INFORMATION: n equals a, t, g or c	PEATURE: NAMENEY: misc_feature LOCATION: (55369). (55369) OTHER INFORMATION: n equals a, t, g or c	NAMA/ROS: misc_feature NAMA/ROS: (65309). (65309) OTHER INFORMATION: n qualbs a, t, g or n	FARIURA NAMB/KRY: misc feature LOCATION: (65313). (65313) OTHER INFORMATION: n equals a, t, g or c

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          PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FLING DAFF: 2006-10-0
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
NUMBER: OF SEQ ID NOS: 658
SOFTWARE: Parentin version 3.0
LENGTH: 870
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Job time : 124.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-969-708-530
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Patent No. USO.05012512A1
APPLICATION ANGED TO Recent Research Application and Therapeutic Screening Using Signaturing OF INVESTIGNT OF USO.05012 OF 
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Pred. No. 6.8e+02;
0; Mismatches 1; Indels 0; G
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOOS CDNA LIBRARIES
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LOANTER: MISSA21 . (145942)
OTHER INCOMMATION: n equals a, t, g or c
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CURRENT APLICATION WINDER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR RAPLICATION WINDER: US/09/215,076
PRIOR FILING DATE: 1999-01-08
NUMBER OF EDQ ID NOS: 38054
SOFTWARE: PRACESO for Windows Version 3.0
SEQ ID NO 925
NAME/KEY: misc_feature
LOCATION: (145171). (145171)
OTHER INFORMATION: n equals a, t, g or c
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Publication No. US20030073623A1
GENERAL INFORMATION:
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2127151 (2001)
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3201 Carnegie Ave, Cleveland, OH 44115,
TEL: 216 431 9900
Fax: 216 361 9596
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(http://www.luddig.org.br/dcriptin/gethtml2.pl?ti=££2=MR3-SN067-240
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I Chasea Leo'46)

The arrington, J. J. Sherf, B. Rundintt, S., Jackoon, P. D., Perry, R., Carn, S., Leventhal, C., Thornton, M., Ramachandran, R., Whitington, J. Lerner, L., Costanzo, D. McElligott, K., Boozer, S., Mays, R., Smith, Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, Le., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, Craston of genome-wide protein expression libraries using random activation of gene expression

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Ada.ref="azano:1866"

Acel Inne="Hibersys Rade Library"

Acel Inne="Hibersys Rade Library"

Ance="Se - Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression

Macure Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."
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3101 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Tel: 216 431 9596
Email: scalmeathersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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nes 21; Conservative
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ORGANISM

AUTHORS TITLE REFERENCE

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666 bp mRNA linear EST 22-JUL-2002 EST613637 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STWG192 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: potato@tigr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
//tissue_type="mixed tissues" / Ala host="SOLR"
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Pax: (106) 516-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plates 3653 row: M column: 4
                                                                                                                                                                                                              Class: BAC ends
High quality sequence stop: 561.
Location/Qualifiers
1. 561
Acquaism=Homo sapiens"
Ab xref="texto:9606"
/clone=plate=3053 Col=4 Row=W"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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Other_ESTS: ESTGif1618
Contect: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjte"
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                                                                                                                                                                                 Seq primer: T7
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HS 3053 A2 GO2 T7C CIT Approved Human Genomic Sperm Library D Homo Applens genomic clone Plate=3053 Col=4 Row=M, DNA sequence.
A0785399 I GI:5693563
GSS.
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1 (bases Lorda, Primates, Catarrhini, Hominidee, Homo.
Waharras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Matler, P., Eurlong, J., Young, J., Zhao, S., Adams, N.D. and
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                             Enklaryota (Metazoa, Chordata, Craniata, Vertebzata; Euceleostomi, Mammala: Eucheria, Rodentis, Sciurogashi, Muridae, Murinae, Mus. 1 (Acap Ence), //www.ncbi.nlm.nih.gov/nciogap.
                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMTGE Consortium (info@image.llnl.gov) for further information.
MGI:1090541
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High Throughput Sequencing center
University of Washington
401 Queen Anne Avenue Morth, Seattle, WA 98109, USA
Tel: (206) 616-3618
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Cdlone="IMAGE:3414729"
Cdlone=lib="Soares mouse 3NbMS"
(sex="male"
                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Other EGTs: uv93dbs.xl
Contact: Robert Strausberg, Ph.D.
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/strain="CS7BL/6J"
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Location/Qualifiers
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BASE COUNT ORIGIN

Hood, L.

JOURNAL MEDLINE

TITLE

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KEYWORDS SOURCE ORGANISM

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mRNA sequence.

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BG595346 potato.

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(db_xec="texton:966"

Aclone lib="myn0109"

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profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under the stringency conditions."

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Arrive 1: Smal; Amini-library was made by cloning products for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under the stringency conditions."
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Final: asimpson@ludwig.org.br
Finis sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be eeen in the following URL
Finis entry can be eeen in the following URL
900-200-FileLisa2000-09-12st=1)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi, Mamaalia, Enteleostomi, Mamaalia, Enteleostomi, Indensia, Enteleostomi, Indensia, Enteleostomi, Mamaalia, Enteleostomi, Marcia, Cortia, Correa, R., Verjovski-Almeida, S., Brones, M.R., Magai, M.A., da Silva, W. Jr., Espo, M.A., Bordin, S., Costa, P.F., Enteleostomi, E., Costa, P.F., Buther, P., Matsukua, A., Bad, G.S., Simpson, D.H., Grunden, A., deoliverin, P.S., Buther, P., Jongenes, C.V., and J. Soates, P. Reta, M. C., Soates, P. S., Simpson, D.H., de Souza, S.J., and definitions of the state of the sta
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1. (Dases 1 to 358)
MCT-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Umwor Gene Index
Ompublished (1997)
Ontect: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Labotastory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Fax: +55-11-2707001
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87.6%; Score 18.4; DB 14;
Best Local Similarity 95.0%; Pred. No. 6.1e+02;
Best Local Similarity 95.0%; Mismatches 1;
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1 ACTITATCCAATTTCACACA 20

Query Match Best Local Similarity 95.01 Matches 19; Conservative

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BASE COUNT ORIGIN

BF092401.1 GI:10898215

DEFINITION

ACCESSION VERSION KEYWORDS

BF092401/c

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human. Homo sapiens

SOURCE

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Makayoda, Metazoa; Chordata; Craniata; Vertebrata; Elteleostomi; Memmalia; Eltheria; Elteleostomi; Memmalia; Eltheria; Promidae; Homo.

Dias Breco, E. Garcia; Princara, Verjovski-Almeida, S. Briones, M.R., Nagai, M.A., da Silva M. Ur. 28go; M.A., Bordini, S., Costa; P.F., Raspai, M.A., Bordini, S., Costa; P.F., Massura, M.A., Raspai, G.S., Simpson, H. Brunstein, A. deoliveita; P.S., Bucheruma, A., Bardini, A., deoliveita; P.S., Bucheruma, A., Sogarea, C.S., Simpson, H. M., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J., and Elipson, A. M., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J., and
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MM4-STD240-100301-034-dl1 ST0240 Homo sapiens CDNA, mRNA sequence.
BEG48187
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                               /note="Organ: sperm; Vector: pBeloBACll; BAC Clones in E-Coli DH10B"
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Best Local Similarity 90.5%; Pred. No. 99+02.
Best Cocal Similarity 90.5%; Pred. No. 99+02.
Mismatches 19; Conservative 0; Mismatches 2; Indels 0
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/ AD xref=raxon;9606"
/ Loome=lythAGE;143819.
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/ Loome=lythAGE;143819.
/ Loome=lythGE;143819.
/ Loome=lythGE;14
                           Emmert-Book, M.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., CONA. Library Preparation: M. Bento Soares, Ph.D., CONA. Library Preparation: M. Bento Soares, Ph.D., CONA. Library Arrayed by: Greg Lennon, Ph.D., Cona. Sequencing by: Mashington University Genome Sequencing Center Dine distribution: NGT-GGAP clone distribution information can be infoomed through her I.M.A.G.E. Consortium/LiNiu, send email to: infoomed overall poor quality
Seq primer: -40UP from Gibco.
High quality sequence actop: 1.
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Makaryoca, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamaalia; Eutheria, Primates, Catarrhini; Hominidae; Homo.
I Dases 1 to 380)
Mahairas, G.G., Wallace, J.C., Smith, K., Saartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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1 Similarity 90.5%; Pred. No. 9.8e+02; Length 358;
19; Conservative 0; Mismatches 2; Indels 0
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High Throughput Sequencing Center
University of Washingtoning Center
(200 Gueen Anne Avenue North, Seattle, WA 98109, USA
Tel: (200 616-8618
Eax: (200 616-8618
Eax: (200 616-8618
Eax: (200 616-8618)
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/organism="Homo sapiens"
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Email: asimposimaludwig.org.br
Pris sequence was derived from the PAPESP/LICR Human Cancer Genome
Pris sequence was derived from the following URL
Pris entry organ be seen in the following URL
900-012-305513-2000-09-1364-1)
900-012-305513-2000-09-1364-1)
Seq primer: pur 18 forward
High quality sequence stop: 427.
Meammalia; Butheria; Primates; Catarthini; Hominidae; Homo.
1. (Assail 10. 427)
Jas Neco, E., Catcia Correa, R., Varjovski-Ahmeida, S., Briones, M.R., Nagail, M.A., Gatcia Correa, R., Varjovski-Ahmeida, S., Costa, P.F., O., O., Costa, P.F., C., Codman, C., Carvalho, A.F., Hasskuma, A., Bala, G. Simpson, D. H., M.J., Sacres, P., S., Bucher, P., Jongenesl, C. Simpson, M. W.J., Soares, P., Brentani, P. S., Bucher, P., Toggenesl, C., V., O'Hare, M.J., Soares, P., Brentani, R.R., Rels, L.F., de Souza, S. J., and Simpson, A.J.
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Use of a random BAC End Sequence Database for Sequence-Ready Map Unpublished (1998)
Unpublished (1998)
Coher, GSSer, CIT-HSP-2137A2, TR
Contact: Mark Adams
Department of Eukaryotic Genomice
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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0; Mismatches 2;
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Fax: +55-11-2707001
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               Length 389;
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Lita Annenberg Hazen Genome Sequencing Center
Local Spring Harbor Laboratory
PO. Box 100, Cold Spring Harbor, NY 11724, USA
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     Ouery Match 84.8%; Score 17.8; DB 13; Best Local Similarity 90.5%; Pred. No. 16+03; Marches 19; Conservative 0; Mismatches 2,
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Plate: zb64 row: f column: 06
Seq primer: -40M13RevUniv
High quality sequence stop: 396.
Location/Qualifiers
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Matches 19, Conservative
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Fax: 516 367 8874
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DEFINITION

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VERSION KEYWORDS

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ORGANISM

BASE COUNT

ORIGIN

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G.J.

TITLE JOURNAL COMMENT

FEATURES

dog

ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

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DEFINITION

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Score 17.8; DB 17; Length
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AG. 2063 BD BDA LInear GSS 16-JUL-1999
HG_2063 BD BD ATC CIT Approved Human Genomic Spern Library D Homo
sapiens genomic clone Plates-2063 Col=6 Row-ED, DRA sequence.
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 9712 Medical Center Dr., Rockville, MD 20850, USA 978 1938 0200 Basai 30 0300 Basai 3
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/gecs="male"
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Best Local Similarity 90.5%; Pred. No. 1ee03;

Best Local Similarity 90.5%;

Matches 19; Conservative 0; Mismatches 2; Indels 0

Matches 19; Conservative 0; Mismatches 2; Indels 0
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BOHKK72TF 603282642 BOMPT62TR Tetraodon

BI656335 BH738785 AL267972 AY109642 BH644242 AW863544

Fugu rubr kp79g12.y UI-R-CA1-

BJ089942 BJ089942	BJ448109 BJ448109	BJ064176 BJ064176 AG095094 Pan trodl	BB620211 BB620211	BM206425 C0297D07-	AZ570619 276PvE11	AL796128 AL796128	BQ402797 GA EG005	BE261578 601149289	BF071772 db57g11.x	BB622794 BB622794 BH040661 BDCT-24-3	BQ413226 GA_Ed007	AQ263171 CITBI-E1-	AG095529 Pan trod1	BI412552 602990859	BJ475913 BJ475913	BF231745 de92c06.x	AZ084741 RPCI-23-3	B1650200 603296292	AW/0/294 JAAUU0631 RH062950 RPCI-24-3	BE303505 601086611	BJ476439 BJ476439	AV918005 AV918005	AZ981579 ZM0262L03	BM072946 MEST56-C1	AL241877 Tetraodon	BF695254 602080491	BG480838 602529967	B12696 F2/NS-1/ 1G BF232885 602023913	BG173194 602335576	B1078173 602872492 A1409998 T3 end of	BG114301 602286063	BF300260 602032168	BQ936776 AGENCOURT	BF233254 602023613 BTE19758 603062042	AL276794 Tetraodon	AL515482 AL515482	AL401204 T3 end of	BO964998 AGENCOURT	AL437536 T7 end of	BG246761 602360839	AL410137 T7 end of	AL413906 T3 end of	AY109642 Zea mays	BC026814 Mus muscu	AF219030 AF219030	AW652251 100108 MA	BI898910 480710 MA	AW336599 22643 MAR AW336608 22641 MAR	AA691655 VS13b11.r	BM030805 495326 MA	AI925100 wn50a01.x	.BB151351 BB151351
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## ALIGNMENTS

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Enail: Gapber-Genail Infl.gov
Tisque Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tisque Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Browner Ph.D.
CON Library Preparation: M. Bento Soares, Ph.D., M. Patima
                                                                                                                                                                                                                                                                           Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       A1962650 HNA linear EST 08-MAR-2K wdg42603.X1 NCI CGAP GCS HOmo saplens cDNA clone IMAGE:2473948 3' similar to 8N:MINK HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN ; "MRNA sequence."
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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DNA Sequencing by: Washingron University Genome Sequencing Center
Clone discribution. NGT-CGAP clone distribution information can be
Glone direction. Let I.M.A.C. Consortium/LLNL at:
www-bio.lln.gov/bbrp/image/image.kml
Insert Length: 770 Std Error: 0.00
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1 (Dessel to 423) colinimini, gov/ncicqap.
NCT-CSAP https://www.ncbi.nlm.nih.gov/ncicqap.
Netional Cancer Cannome Anatomy Project (CGAP).
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Bhail: cgapbe-Ydmail.nih.gov
Than Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmetr Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1654552 429 bp mRNA linear EST 17-DEC-18 wb4bBl2.x1 NCI CGAP GC6 Homo explains cDNA clone IMAGE:2308895 3' similar to 68:MINK HUMAN P15382 ISK SLOW VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 GACGICITCCGAAGGATTTTTATTACTTATAGGACAATTGGCGCCAGAACACAACAGCT
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Pred. No. 1.7e-71;
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100.0%; Pred. No. 1.
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/lab host-"Hills"
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/hoct="DRH108"

/hoct="Organ: mixed (see below); Vector: pT773D-Pac

(Pharmacia) with a modified polylinker; Site 1: Not I,

Site 2: Eoc Ri, Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 20kHW, pregnant uterus

NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vittor. Pollowing hAPP purification, this DNA

was used as tracer in a subtractive hybridization.
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3' similar to SHFAINK HUMA N B15382 ISK SLOW VOLTAGE-GATED POTASSIUM
FEANNEL PROTEIN ;, MRNA sequence.
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Mamalla; Butheria; Primates; Catarrhini, Hominidae; Homo.
1 (bases 1 to 391)
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| Lab zref="razon:1966" |
|clone="TwAgE:195156" |
|clone=lib="Soares NhiWPD.Sl" |
|fissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
This close is available troyalty.free through LLNL; contact the This close is available troyalty.free through LLNL,; contact the INAGE Conscrtium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.
High quality sequence estop: 380.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CCGAAGGATTTTTATTACTTATATGGACAATTGGCGCCAGAACACAACAGCTGAGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 GGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCTGTACCTCATGGT
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AI339609.1 GI:4076536
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Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 bp mRNA linear EST 28-JAN-1999 q15994.x1 Soares NhiMPL S1 Homo appiens cDNA clone INAGE:1857942 3' similar to 58:NINK HUMAN P1382 ISK SLOW VOLTAGE-GATED POTASSIUM AT246219 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCAAGAGGCCCTCCAAGCCAAAGTTGATGCTGAGAACTTCTACTATGTCATCCTGTAC 150
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) Cyganism="Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Bmall: Gapber Famell.nih.gov
This Glone is available royalty-free through LLNL; contact the
This Glone-time finice@image llnl;gov) for further information.
Thaert Length: 921 Std Error: 0.00
Seq primer: -40TP from Gibco
High quality sequence etop: 365.
Location/Qualifiers
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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www-bio.llnl.gow/bbrp/image/image.html
Innert_Langth: 71 Std Error: 0.00
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High quality sequence srop: 411.
Location/Qualifiers
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Unpublished (1997)
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1. Organism - Homo sapiens"

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                                                                                                                                                                                                          BG221966 746 bp mRNA linear EST 21-APR-2001 RST41783 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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Harrington J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry R., Cans, S., Leventhal C., Thornon, W. Ramachandran, R., Whitington, J., Lerner, M. Kilka, A., Hess, J., Cothen, K., Lo, K., Maya, R., Smith, E., Danson, J., and Ducar, H., Escher, Cothen, R., Lo, K., Offenbacher, C., Danson, J., Danson, J., Danson, J., Danson, J., Cothen, R., Lo, K., Offenbacher, C., Caston of genome-wide protein expression libraries using random activation of gene expression

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Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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           557 AGAACTTCTACTATGTCATCCTGTACCTCATGGTGATGATTGGAATGTTCTTTCA 501
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100.0%; Pred. No. 6.5e-35;
.ive 0; Mismatches 0; Indels
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3201 Carnegie Ave, Cleveland, OH 44115,
Tel: 216 431 9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 547.
Location/Qualifiers
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BG221966.1 GI:13747987
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AW869303.1 GI:8003356
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Best Local Similarity
Matches 84; Conserv
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/db_xxet=raxon:9606"
/clone lib="Athereys RAGE Library"
/cell_lib="HT1080"
/nocle="See 'Creation of Genome-wide Protein Expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGACAATTGGCGCCAGAACACACAGCTGAGCAAGAGGCCCTCCAAGGCCAAAGTTGATGC 122
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exection. The driver wau PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools confisted to 5.1.H.A.G.E. Clones 23.2-265223, and 464848-489479."

140408-349479, and 464848-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TGAGAACTTCTACTATGTCATCCTCTGTGGTGATGATTGGAATGTTCTCTTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cruniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG208163 803 bp mRNA linear EST 21-APR-21 RST27654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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Best Local Similarity 100.04, Pred. No. 6.6-5.7
Matches 117; Conservative 0, Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                              Length 391;
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                                                                                                                                                                                                                                                                                              Score 119; DB 9;
Pred. No. 4.8e-54
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Tel: 216 431 9900
Fax: 216 361 9596
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21227151
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG208163.1 GI:13729850
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 119; Conservative 0
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Eax: +55-11-2707001
Fax: +
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/ Clone lib=180005**

/ Adv Gages**Adular*

/ Adv Gages**Adular*

/ Ance=Corgan: stone normal; Vector: puc18; Site 1: Smal; Site 2: Smal; A min; Library was made by cloning products derived from ORESTS PCP (U.S. Letters Patent application No. 196, 716 ** Lidwig Inttilute for Cancer Research); Deptilles into the DW C10 vector. Reverse transcription of tissue mRNA and CDNA, amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Struewesty, Ph.D.
Bmall: cgpbb-r@mail.nih.gov
Bmall: cgpbb-r@mail.nih.gov
Bmall: cgpbb-r@mil.nih.gov
Bmart-Buck, M.D., Ph.D., Michael
Bmart-Buck, M.D., Arryed by Greg Lemon, Ph.D.
DNA Library Arryed by Greg Lemon, Ph.D.
DNA Staryed by Greg Lemon, Ph.D.
DNA Staryed by Mashington University Genome Sequencing Center
Clond distribution, NGI CGAR Clone distribution information can be
found through the I.M.A.G.E. Consortium/Linkl at:
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NCI -GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Mational Tannear Institute, Cancer Genome Anatomy Project (GGAP), Tumor, Ogne, Index.
        Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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miniar co SH-MIWK HUWAN b15382 ISK SLOW VOLTAGE-GATED POTASSIUM
CHANNREL POOTEIN ;, mRNA sequence.
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nes 0;
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Insert Length: 763 Exd Error: 0.00
Seq primer: -40m13 Fwd. ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bmail: asimpsonsludwig.org.br
This sequence was derived from the FAPBSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(Inttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=£t2=MR3-SN0067-240
Seq primer: puc 18 forward
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11. (Basea I to 311)
12. Basea I to 311)
12. Marca (Barrinia); Verjovski-Almaida,S., Briones, M.R., Magai, M.A., da Silva,W. Jr., Zago,M.A., Berdin,S., Costa,F.F., Mateukuma,A., Bario,S., Simpson,D.H., Brunstein,A., deoliveira; S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentan,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                     Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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20202663
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 11 High quality sequence stop: 74.
                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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                                                                                                     Simpson, A.J.
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Best Local Similarity
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AW869303
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/organism="Homo sapiens"

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Mammalla, Buthbria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 1003)
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Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/clone lib="Rat 21 day old female ovary mRNA PMSG 3h"
/sex="female"
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National institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
                                                           Gaps
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/dev_stage=-1,1 day old
/note="tissue_type=hypochalamus; dev_stage=adult_rat"
127 c 128 g 95 t 4 others
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16.6%; Score 30; DB 13; Length 351; 100.0%; Pred. No. 1.6e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute for Molecular and Cellular Reg
Gunna Univ., Bloaginal Research Center
Shouwa machi 3-39-15, Macbashi, Gunma 371, Japan
Email: tmizu@sb.gunma-u.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyamoco, K., Mizucani, T., Numata, Y. and Okada, T. Rat 21 day old female ovary mRNA 'Unpublished (1996) Contact: Miyamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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100.0%; Pred. No. v.
0; Mismatches
                                                                                                                                          247 GTTGATGCTGAGAACTTCTACTATGTCATC 276
                                                                                                                115 GTTGATGCTGAGAACTTCTACTATGTCATC 144
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Matches 26; Conservative
       Query Match
Best Local Similarity 100.0
Matches 30; Conservative
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/ (Alone_INAGE.1871680"
/ (Clone_INAGE.1871680"
/ (Clone_INAGE.1871680"
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IAbol4A12 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
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Mamalla; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Bages 1 to 351)

Woore, S. S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G.
CDNA, B from bovine abonesum tissue
Unpublished (2001)
Unpublished (2001)
Contact: Dr. Stephen Moore
Contact: Dr. Stephen Moore
Dont of RNS, University of Alborta
410 Agri/For. Dept of ARNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Eax: 80 429 4265
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                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 35; DB 9; Length 121; 100.0%; Pred. No. 2.6e-08;
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Seq primer: T3 primer
High quality sequence stop: 351
POLYA=No.
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           xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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FORWARD: M13 Forward
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States J. Shinagawa.A. Shibata.K. Yoshino.M. Ichi.M. Ishiiy, Araka.a. T. Bara.A. Rokuinishiy. Yoshoo H. Macch.J. Fukuda.S. Arawa.M. Nahi.K. Rokuo.B. J. Fukuda.S. Arawa.M. Nahi.K. Rokuo.B. J. Fukuda.S. Salota.M. Nahi.K. Mondo.H. Ksalota.T. Salot.R. Salota.M. Rokuda.A. Salota.M. Fastobami.M. Gasasellad. T. Gissi. C. King.B. Nochwa.H. Kohin. M. Bacalovi.S. Casavani.T. Nahi.M. Pescia.G. Salota.H. Macch. M. Salota.M. M. Salota.M. M. Salota.M. M. Wagneri.L. Washoo.T. Salota.M. M. Wagneri.L. Washoo.T. Salota.M. M. Salota.M. M. Wagneri.L. Mono.H. M. Salota.M. M. Wagneri.L. Mono.H. M. Garinod.M. M. Garinod.M. M. Boluma.M. M. Mani.M. M. Garinod.M. M. Mani.M. M. Garinod.M. M. Mani.M. Mani.M. M. Mani.M. M. Mani.M. M. Mani.M. M. Mani.M. Man
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Nature 409 (6821), 685-690 (2001)
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/db_xref="MGD:MGI:1901204"
Genome Res. 10 (11), 1757-1771 (2000)
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    /organism="Mus musculus"

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/clone="2200002116"
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BRNA linear HTC 19-JAN-2002
When meculius adult male stomach Chon, FAKEN [Lill-length enriched library, Cone: 2200002116: homolog to MINHUM POTASSIUM ION CHANNEL-RELATED PERFIDE 1 (MIRP1) (MINK-RELATED PERFIDE 1), full
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Site_2: Sall; Cloned undirectionally, oligo-GT primed. 
Average insert size 3.3 kb. Library enriched for 
full-length clones and constructed by Life Technologies. 
Note: this is a NIH MGC Library.*
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MNB musculus (strain:CS7BL/6J) adult male stomach CDNA to mRNA, clone_lib:RISM Full-length enriched mouse cDNA library close=2200002116.
cDNN Library Preparation: Life Technologies Inc.
MNL Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNN Sequencing by: They'e Generica.

Note distribution: MGC close distribution information can be found through the IN.A.G.E. Consortium/LLNL at:
Plate: LLMNU316 row: g column: 22
High quality sequence stop: 535.

Location/Qualifiers
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/tissue type="retina"
/lab_host="DH10B (phage-resistant)"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4481325"
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H77654 Soares fetal liver Spleen INFLS Homo sapiens CDNA clone
TMAGE:234137 3', mRNA sequence.
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                                                     Carninci.P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999] [1999]
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/dom_xref=vaxon:10090"
/clone="xorox1se"
/clone="xorox1se" full-length enriched, adult male
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/dev_stage="adult"
/lab_host="SOLR"
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Thermostabilization and thermoactivation of thermolabile enzymes by
tremostabilization and thermoactivation in synchrometers of full length
Tengalo.iv. Garninci.p., Sibbata.iv., Ozaway.y., Muramateu.M., Okazaki.iv.
Automated filtration-based high-throughput plasmid preparation
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BBS64873 RIKEN full-length enriched, adult male stomach Mus
museculus CDNs clone 2200002116 5', mRNA sequence.
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/dev_grage="adult"
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Laboratory for Gonome Exploration Research Group, RIKEN Genomic
Science Center(GGV), Vokohama Instituted Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cnb, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-033-922
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Zhao, S., Shetty, J., Shatsman, S., Taegaye, G., Geer, K., Shvartsbeyn, J.A., Gebrageotgian, B., Overton, L., Riusell, D., Chen, D., Riggs, F., de brageotgian, B., Overton, L., Riusell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Unpublished for als Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)

Contact: Shaying Zhao
Department of Bharyotic Genomics
Department of Bharyotic Genomics
Department of Charyotic Research
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Srinivasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddarz, Srinivasan, J., Sinz, W., Kipping, I., Pires da Silva, A., Jesse, T., G., WitterH., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T., A. BAC-based genetic linkage map of the nematode Pristionchus pacificus.
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Contact: Sommer RJ
Prolutionary Biology
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Spenanner: 37.13, Tuebingen D-72076, Germany
Fax: 04997071601371
Fax: 04997071601498
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6., Witter, H., Keller.H., Kipping.I., Piree da Silva.A., Jesse.T.,
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Brollationary Biology
Max-Panck-Institute for Developmental Biology
Spemanner. 37-59. Trebingen D-72076, Germany
Tel: 00497071601499
Exx: 00497071601499
Bmail: xalf_sommer@tuebingen.mpg.de
Insert Length: 968 Std Error: 0.00
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Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
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//organism="Homo sapiens"
/clone="C300H005Y023"
/clone=lib="trl FL012 TC1"
/tissue="rype="T-cells from T cell leukemia"
/lab_hoge="T-cells from T cell leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 19; DB 9; Length 938; 100.0%; Pred. No. 19;
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Location/Qualifiers
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Matches 19; Conservative
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                                              Fax: 301 338 0208

Fax: 301 338 0208

Fax: 301 338 0208

Clones are derived from the rat BAC library CHORL-230

Clones are derived from the rat BAC library CHORL-230

availability, plesse contact Pieter de Jong (pdcjongemal.cho.org).

Clones may be pirchased from BACBAC Besourced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Citions are desired from the rat BAC library CORR-12) availability please contact Fretild html For BAC library availability please contact Finter de Jong (pdejong@mail.cho.org). Clones may be purthased from BACPN Resources (fitter) from Firthy from English English (fitter) from Firthy from Fir
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CH220-8514, DNA sequence.
EH30248, DNA sequence.
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//ecc."Female"
CHOR1-Lypp="Brain"
CHOR1-230 Rat (BN/SBNHad/MCM) BAC library produced by
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.igr.org/bacpac/or ering_information.htm)
Plate: 44 row: E column: 10
Seq primer: 77
Class: BAC ends.
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      Medical Center Dr., Rockville, MD 20850, USA
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/clone_lib="CHORI-230 Sngment 1"
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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C
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Class: BAC ends
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalara Futheria, Rodentia, Solivophath; Muridae, Murinae, Mus. Romon, A. Akabira, S., Akiyama, J., Carninci, P., Endo, T., Futhka, S., Fukuishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, W., Izawa, M., Kadora, K., Kagawa, I., Kai, C., Kawai, Y., Kikuchi, N., Kojima, Y., Koya, S., Kisshade, M., Macsayama, T., Micher, R., Misuno, Y., Nakamuza, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Shibata, Y., Shigemoto, Y., Shibata, Y., Soghe, S., Shighata, Y., Shibata, S., Suzuki, H., Takhashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watanabo, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabo, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabo, H., et al., 1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Immature ear; Vector: ZAP Express (pBK-CMV); Site 1: ECORT; Site 2: Xho1; RNA from library 606 was filtered for Common ESTE found in 606."

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Contact: Yochikide Hayashizaki
Dabotatory for Genome Rayloration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokobana Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokobama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                         /db xref="taxon.4877"
/clone.lb="853 - Immature ear with common BSTs screened
by Schmidt lab" clonescence meristem - floral organ
primordia"
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musculus CDNA clone 7420430N10 3', mRNA sequence.
AVJ58849
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                                      Wallot, V. Maize ESTs from various cDNA libraries sequenced at Stanford
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                                                                                                                             Contact: Walbotr V
Department of Biological Sciences
Stanford University Palo Alto, CA 94304, USA
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 773 2237
Fel: 658 8221
Fendli: walboce@stanford.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
  clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="0.5 cm to 2 cm"
/lab_host="Stratagene XLOLR"
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100.0%; Pred. No. 51;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                   Plate: 953004 row: F column: 12.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 bp
                                                                                                                                                                                                                                                                                                                                                  /organism="Zea mays"
/cultivar="OH43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 ACCCTGGAAGACGTCTTC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ACGCTGGAAGACGTCTTC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV358849.1 GI:6405851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.99
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                        Unpublished (1999)
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                                                                                      University
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AV358849/c
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ORIGIN
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                    REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 bp mRNA linear EST 28-JAN-2002 953004F12.x2 953 - Immature ear with common ESTs screened by Schnidt lab Zea mays CDNA, mRNA sequence.
BM16658-1 GI:1838365R
                                         34644242 1008 - 139 bp DNA linear GSS 14-FEB-2002 1008056H01.xl 1008 - RescueMu Grid I Zea mays genomic, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                    Maize genomic sequences found using engineered RescueMu transposon Monblished (2001)
Contact: Malbot V
Contact: Malbot V
Spartment of Balogical Sciences
Stanford University
855 California Ave, Pelo Alto, CA 94104, USA
Fas: 650 723 222,
Fas: 650 725 822,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zee mays
Bhkaryoca, Viridiplantae, Streprophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, PACC
                                                                                                                                                                                                              Enkaryota, Viridiplantae; Streptophya; Embryophyta; Tracheophyta;
Spemacophyta; Magnoliophyta; Lilopsida; Poales; Poaceae; PACC
Spade; Panicoideae; Andropogomea; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon_4577"

/db_xref="taxon_4577"

/tissue_type="leaf"

/dow_trage="adult"

/lab_host="billing"

/note="Organ: leaf; Vector: RescueMu (engineered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1008056 row: 5
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Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultivar="mixed background W23/A188/B73"
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les 18; Conservative 0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Zea mays"
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                                                                                                                             BH644242.1
                                                                                      sequence.
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                                                                                                                                                                                               Zea mays
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ORIGIN
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BM416858/c
                                                                                                                                                                    SOURCE
ORGANISM
                                         COCUS
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AUTHORS
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                                                                                                     ACCESSION
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RESULT 21
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KEYWORDS
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KEYWORDS
SOURCE
                    3H644242
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Email: genome-res@gsc.riken.go.jp,

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AA984762 am90gOZ.sl Stratagene schizo brain Sil Homo sapiens cDNA clone NAKAE:1630418 3', mRNA sequence.
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Hillier.L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Hillier.D., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Karaman,D., Kuobba,T., Leavy,M., Len,K., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryc, heart, muscle, spleen"
/lab host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; Estimated insert size approx.1 kb"
101 c 109 q 107 t
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watcon,wustl.edu
This clone is available royalty-free through LLNL; contact the
TNAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyn not found
Seq printer: -40ml3 fwd. ET from Ameraham
High quality sequence scop: 414.
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                                                                                                                                                                                                                                                                     contact the ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 18; DB 10; Length 401; 00.0%; Pred. No. 58;
                                                            Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, t
9712, Medical Center Drive, Rockville, MD 20850, t
761: (301)-838-3259
Fax: (301)-838-0208
Easi: nhies@tigr.org
This clone is available through the ATCC, contact
tel#703-356-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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/clone="YMAGE:1630418"
/clone="YMAGE:1630418"
/eac="male"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.34; ccccc 59; Best Local Similarity 100.0%; Pred. No. 58; Best Local Concervative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse.
Location/Qualifiers
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                                Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                        .401
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JOURNAL
COMMENT
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AA984762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anoie "Signe 1: Salte," I salte, 2 and its count library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genome Carolic Statement of Carolic Statement and Genome Science Libraratory in RIKEN. Division of Exportmental Animal Research in Riken contributed to prepare mouse tissues: its transchold was prepared by using trehalose there is such a first an exclusion of Exportment and Carolic Statement an
                                                                                                                    Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Scil. V.S.A. 95 (7), 345-3460 (1998) ICDh.M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Shibata, Y. Cawa, Y., Muramatsu, M., Okazaki Almonated filtration-based high throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was cloned into the XhoI and BamHI gites. Vector: a modified paluescript KR(+) after bulk excision from Lambda FLC I. Cloning sites, 5, end: Sall; 3, end: BamHI"
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URL. http://genome.gec.riken.go.jp/
asaki.W. Izawa.M. Wetaniki.M. Ozawa.K.. Tanaka.T., Yoneda.Y.,
Marguuta.S., Carninci.P., Muramateu.M., Okazaki.Y. and Hayashizaki
Ageguuta.S., Carninci.P., Muramateu.M., Okazaki.Y. and Hayashizaki
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Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 401)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.rtc.riken.go.jp) for
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/clone="742030N10"
/clone=1ib=RXKEN full-length enriched, in vitro
ferti]Ized_eggs"
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trissue_type="in vitro fertilized eggs"
dev_stage="egg"
lab_nost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C578L/6J"
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 C
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Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details
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AL040827
DKEZPA4F1615_r1 414 (synowym: htes3) Homo sapiens cDNA clone
RKEZp44F1615_r1 414 (synowym: htes3) Homo sapiens cDNA clone
RKEZp44F1615_5', mRNA sequence.
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Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales; Pabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinaried, Germany
This is the S. sequence of the Globa insert.
Clone from S. Wieman, Molecular Genome Analysis, German Cancer
Clone from S. Wieman, Molecular Genome Analysis, German Cancer
Clone from S. Wieman, Molecular Genome Analysis, German Cancer
Sequenced by GBP (Mational Research Centre for Biotechnology Ltd.,
Braunschweigldgermany) within the CDNA sequencing consortium of the
German Genome Project.
What S. Clone (DMFZ944F161s) is available at the RZPD in Berlin.
Please contact the RZPD: Reseourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ekkaryota; Metazoa; Chordata; Craniata; Vertebrata; Bureleostomi;
Mammalis; Butheria; Primates; Catarrhini; Hominidae; Homo
I i Dases I to 425)
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50 g 120 t
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/clone="DKFZp434F1615"
/clone_lib="434 (synonym: htes3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                 70
                                                                                                                  45 TTACTTATATGGACAATT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE941069
BE941069.1 GI:10518828
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Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                           AL040827.1 GI:5409772
                                                 53 TTACTTATATGGACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 471)
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AL040827/c
LOCUS
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ORGANISM
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Louding the Ass. Beliaville Agricultural Research Center Bidg. 200 Ms 21, Beliaville, MD 20705, USA Tel: 301 504 8414

Fax: 301 504 8414

Fax: 301 504 8414

Fax: 301 504 8414

Fax: 101 50
/dev casega-"34 years old"
/lab_host="SGOJM (kanawycin resistant)"
/loce="wetore: Bluescripts KX-, Site_1: EcoR1; Library
/noce="wetore: Bluescripts KX-, Site_1: EcoR1; Library
/noce="wetore: Bluescripts KX-, Site_1: EcoR1; Library
/noce="wetore: Bluescripts KX-, Site_1: EcoR1; Variate
/noce mortand from S-II fronto. Bluescript RI VAD:
/noce mortand from S-II fronto. Was
/noce mortand by obmestor NX- Torrey. E.F. '10 ken R.,
/noce mortand by obmestor NX- Torrey. E.F. '10 ken R.,
/noce mortand realine of Individuals with Perphiatric
/noce mortand realine of Individuals with Perphiat
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Library made from pooled mRNA isOlated from mammary
tissues at eight physiological, developmental, and disease
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10. Veses 1 to 419

Constegati, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/organism="Bos taurus"
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/clone_lib="BARC 5BOV"
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/lab_host="DH108"
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/incfe"Wector: pAMP1 (Gibco); Site 1: NoLf; Site 2: Sall; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Mashington University, St. Louis. The CDNA was made by using Dynabeed oligo-dip Trining (Dynal). PERS based library using a modified protocol from the SMAT PR: CDNA SYRThesis RIX (from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Warwick Grant of AgRearch, New Zealand (Warrick, grantegeresearch. Co.nz).
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2000102.X2 603 - stressed rooc cDNA library from Wang/Bohnert lab
2ea maye 200N, mRNA sequence.
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I (Daess I to 580)

Malbot, V.

Malac ESPS from various cDNA libraries sequenced at Stanford
                                                                                                                                                                     McCarter (bchiapel@watson wustl.edu & jmccartee@watson.wustl.edu)
Mashington University, St. Louis. DRA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 381.
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                                                                                                                                        The library was constructed by Brandi Chiapelli and Dr. James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Parastrongyloides trichosuri"
/db_xref="texon:131310"
/oloe lib="Parastrongyloides trichosuri IL pAMP1 v1
Chiapolii McCarter"
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/clone lib="603 - stressed root cDNA library from
Wang/Bohnert lab"
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/lab_host="DH108"
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Stanford University
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/dev_stage="salt stress"
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/organism≃"Zea mays"
                                                                                           Email: est@watson.wustl.edu
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Email: walbot@stanford.edu
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                 Fel: 314 286 1800
Fax: 314 286 1810
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/tissue type=Woodce from four day old seedlings"
/decems_type=Woodce from four day old seedlings"
/decems_type=Woodce from four the beta glucan
eliding to the four from the four seed from the four from the f
S COCE, Cydanen-Reuths, T., Hahn, M.G., VandenBoach, K., Rur, J., Beremand, P., Endre, G., Town, C.D., Bowman, C.L., Craven, M.B. and Chonson, C.D., Eroman, C.D., Craven, M.B. and Chonson, C.D., Eroman, C.D., C.D., Eroman, C.D., C.D., Eroman, C.D., C.D., Eroman, C.D., C.D.,
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479 bp mRNA linear EST 25-SEP-2001

823.96.3.1 Parastrongyloides trichosuri Li pAMPP v1 Chiapelli

McCarter Parastrongyloides trichosuri cDN 5' similar to MP.CE24272

741C9A.4 glutamate receptor ;, mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Panagrolalmoidea; Strongyloididan; Parastrongyloides.
1 (Dases 1 to 479)
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100.0%; Pred. No. 60;
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Unpublished (1999)
Contact: McCarter JP
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/cultivar="A17"
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Parastrongyloides trichosuri
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Divervotes, Metacoo, Chordata, Craniata, Vertebrata; Buteleostomi; Manalas Butheria; Primates; Gararhini; Hominidee; Homo.

Homes and the costs.

Hattori, M. Ishii, K. Toyoda, A., Shiba, T. and Sakaki, Y.

Home sapiens genome DNA, chromosome 21q

Dublished Only in Database (1998)

Hattori, M. Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

Defert Colonia Short Shipa, Masahira Hattori, Kitasato University, Shipa, Shipa, Shiba, T. and Sakaki, Y.

Department of Stience, OST Sequenting Laboratory, Kitasato 115-1, Sagamhara 22g, Japhn (S-mail Hattori, Kitasato University, Tayanama 22g, Japhn (S-mail Hattori, Mitasato 115-1, Sagamhara 22g, Japhn (S-mail Hattori, Mitasato 115-1, Sagamh
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   Homo sapiens genomic DNA, chromosome 21q
published Only in DataBase (1399)
2 (based 1c 690)
Battori, M., Ishli, K., Toyoda, A., Shiba, T. and Sakaki, Y.
Direct Submission
Direct Submission
Department of Science, JST Sequencing Laboratory, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato Oliversity,
Tel. 10427-18-9732, Fax.10427-78-5561)
On Peb S. 1999 this sequence version replaced gi:2754668.
AG003766; Submitted (17-Jan-1998).
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100.0%; Pred. No. 63;
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/db_xref="taxon:9606"
/chromosome="21"
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/db_xref="taxon:9606"
/chromosome="21"
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/lab host="E. coli XI.Gold"
/note="Vorgan: roots, Vector: pBluescriptII SK(+) XR,
fordean: roots for conx library from Wang/Bohnert lab"
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Homo sapiens genomic DNA, 21g region, clone: T485XN, genomic survey
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Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
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Departent of Science (JST Sequencing imboratory; Kitasato 1-15-1,
Sequencinara 28 olden (E-mail hattor/depg.:hms.u-tokyo.ac.jp,
Telio427-78-9372, Pant. (A-77-78-9561)
Telio427-78-9399 this sequence version replaced gi:2754675.
MG003773: Simbitted (Yo-Jan-1998).
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1. (bases 1 to 632)

Hetcori, M., 18hil, K., 70yda, A., 8hiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q

2. (bases 1 to 682)

2. (bases 1 to 682)

Hattori, M., 18hil, K., 70yda, A., 8hiba, T. and Sakaki, Y.

Direct Submission.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
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Pred. No. 62;
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/db_xref="taxon:9606"
/chromosome="21"
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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AG009962.1 GI:3289948
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AG009955.1 GI:3289941
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Bixassica oleracea.

Bixassica oleracea.

Bixaryoca. Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bixaryoca. Viridiplantae; Streptophyta; endicoryledons; core endicots;

Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.

Town.C.D., Van Aken, S., Utterback, T., and Fraser.C.M.

Whole genome shotgun sequencing of Brassica oleracea

Other_GSS: BOGMT27R
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/clone=100507472"
/clone_lib=1803W
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic_DNA inserted_into pHOS1 using BstXI linkers"
1 180 c 139 g 254 t
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BOGWT27TF BOGW Brassica oleracea genomic clone BOGWT27, DNA
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NPA is from a doubled haploid provided by Tom Osborn.
SE primer: TF
Class: sheared ends.
                                                                                                                                                                             Length 702
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Tel: 301-838-323
Fax: 301-838-0208
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100.0%; Pred. No. 64;
tive 0; Mismatches. 0; Indels
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/strain="TO1000DH3"
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                                                                                                                                                                                              100.0%; Prec. notive 0; Mismatches
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/db_xref="taxon:9606"
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                     /chromosome="21"
/map="21g"
/clone="T485XN"
a 193 c 136
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GSS.
Oryza sativa.
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Matches 18; Conservative
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E. 1 (bases I to 700)

E. Hattori, M. 18hik, T. Toydoa, A., Shiba, T. and Sakaki, Y.

E. Hattori, M. 18hik, K. Toydoa, A., Shiba, T. and Sakaki, Y.

E. 2 (bases I to 700)

E. 3 (bases I to 700)

E. 2 (bases I to 700)

E. 3 (bases I to 700)

E. 3 (bases I to 700)

E. 3 (bases I to 700)

E. 4 (bases I to 700)

E. 5 (bases I to 700)

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E 1 (bases 1.0702)
Hattori, M. 18hii.K., Toyoda, A., Shiba, T. and Sakaki, Y.
Homo sapiens genomic DNA, chromosome 21q
Homo sapiens genomic DNA, chromosome 21q
E 2 (bases 1.0702)
E 2 (bases 1.0702)
E 3 (bases 1.0702)
Direct Submission
Submitted (06-JUL-1999) Masshira Hattorici, Kitasato University,
Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattorichgc.ims.u-tokyo.ac.jp,
Tel:042-78-9732, Fax:0427-79-5561)
CON FED 5, 1999 this sequence version replaced gi:2754672.
                                                                          AG009957 700 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21g region, clone: T485XN, genomic survey
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100.0%; Pred. No. 63;
tive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/chromosome="21"
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Homo sapiens
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/clone="T485XN"
203 c 127
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GSS.
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Matches 18; Conservative
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AG009957 AG003768
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Abackbone of the vector is basically from pBluescript (KS), that was in vivo excised from a modified 1PS phage vector (MO bi Tec, was in vivo excised from a modified 1PS phage vector (MO bi Tec, Germany). 5' and of the coronx that was digested with KNO1 was ligated to Sali site of the vector and the 3' end including polyatall was ligated to BamHI site of the vector. This full length omplified with conventional Ty and Ty pinhers. This full length of MA library was generated basically according to the method described in The Plant U 15, 707-720 (1988) Seki M: e. al.

Protonemants were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13,-14 days under the continuous light.
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Physocontrella parens subsp. patens.
Physocontrella parens subsp. patens.
Bubaryota, viridiplantes; Streppophyta; Embryophyta; Bryophyta,
Bryopsida, Funatidae, Funatzales; Funatzacee; Physoconitrella.
I Obases To 731)
Pullan T. Shhull T. Seki, M. Kamiya, A., Uchiyama, T.
Carninci, P., Haysshraki, Y., Shinosaki, K., Kohara, Y. and Hasebe
Zhang, X. Y., Feng, J., Li, G., Qian, H. N., Li, X. P., Wu, D. C. and Hu, Y. C. Dyfferentially expressed transcripts in ovarial cancer identified by mRNA differential display (Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Homo sapiens ovary epithelium"
/fissue_type="voary epithelium"
/fissue_type="voary epithelium"
/note="Anchor enzyme: Nlail: "This SAGE library is from
Brain
/note="Anchor enzyme: Nlail: "This SAGE library is from
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/note="Anchor enzyme: Nlail: "Library is from
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/note="Anchor enzyme: Nlail: "Library is from
/vogelstein, Brain
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Aymeoologic Gmoology Center
People's Hospital, Beijing Medical University
133 Punel Street, Mestern District, Beijing, 100034, China.
Location/Qualificers
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/db_xref="taxon:145481"
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pupublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Wishima, Shizuoka 411-8540, Japan
Tat: 81-559-81-6855
Pax: 81-559-81-685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="N3A018"
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                                    Midwayora, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Percentophyta, Liliopsida, Poales, Poaceae; Poaceae; Poaceae; Poaceae; Poaceae; Poaceae; Poaceae; Poaceae; Poaceae; Parking, Poaceae; Poaceae; Poaceae; Parking, Poaceae; Poac
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Ekkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 714)
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N3A018, mRNA sequence.
AF136410. G:4969451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29534, USA
Tel: 864 656 7288
Fax: 864 656 4288
Eaxi He 456 429
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Location/Qualifiers
1. 708
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
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Matches 18; Conservative 0;
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/noce_vorcer: pyTTJPAC; Site 1: ECORI; Site 2: NoLI;
/noce_vorcer: pyTTJPAC; Site 1: ECORI; Site 2: NoLI;
ds.cDNA molecules were generated as follows. Fitst-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NoLI oligo-dT primer [5; related mRNA by priming
with a NoLI oligo-dT primer [5; related with RNABB H and used
as a template for DNA poll-catalyzed second strand
synthesis. After the addition of ECORI adaptors, the
ds-cDNAB were diseased with NoLI and size-selected. The
resulting molecules were directionally cloned into the
resulting molecules were directionally cloned
into the
resulting molecules were directionally cloned
into the second of the promable of the pyTTJPAC vector. The library
then went through one round of normalization to CoT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-606, 1996).

NATIC 202 9 111 c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (intrp:)/depre.washington.edu/wentures/collabr/deirce/findex.htm#b
Libry parameters are set to seassament and vector trimming were
conducted using the Lucy software (Ahtrp://www.tigr.org/sofflab/).
Libry parameters were set to ensure an overall trimmed quality of
97.5 to Detter without any vector fragments in the chosen
physy. Detter without any vector fragments in the chosen the
phyyr and the high-quality region were replaced with N's b to serve
phyyr and the high-quality region were replaced with N's b costve
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                                               Bukaryota, Viridiplantae; Streptophyra; Embryophyra; Tracheophyra; Spenatophyra, Magnoliophyra; Lilopaida, Poales; Poaceae; PACC clade; Panicoldeae; Andropogonae; Zea.
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                                                                                                                             (buses 1 to 755)

Olu, F., Cui, P., Guo, L., Aehlock, D.A, Wen, T.J. and Schnable, P.S.

Expressed Sequence Tags from B73 Maize Seedlings and Silks

Unpublished (2001)

Contact: Patrick Schnable

Schnable Laboratory

Tows State University

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA

Tel: 515-294-0799

Email: Schnable@lastate.edu

Email: Schnable@lastate.edu

Email: Schnable@lastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BOHKK72TF BOHK Brassica oleracea genomic clone BOHKK72, DNA
BEQUENCE.
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Query Match

19.9%; Score 18; DB 13; Length 755;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels

Matches 18; Conservative 0; Mismatches 0; Indels
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/clone lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_hods="DH108"
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/cultivar="B73"
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Brassica Officeae
Brassica Officeae
Brasryca, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Buharyota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Brassica, Streptophyta; Magnollophyta; endicoryledons; core endicors;
10 (bases 1 to 736)
Whole ganome abtorn sequencing of Brassica oleraces
Unpublished (2001)
Whole ganome shotgum sequencing of Brassica oleraces
Unpublished (2001)
Chira Casa; Bodyuyare
Contact: Chirs Town
   /clone="pphi3k13"
/clone lib="full length cDNA library, chloronemata and
young gametophores"
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genomic DNA inserred into pHOS1 using BstX1 linkers*
149 c 170 g 149 t
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                                                                             /tissue type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
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DNA is from a doubled haploid provided by Tom Osborn.
Seq prime: TR
Class: sheared ends.
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Pred. No. 64;
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1. 736
/organism="Brassica oleracea"
fstrain="TO1000DH3"
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/clone="BOGIV33"
/clone_lib="BOGI"
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Fax: 301-838-0208
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/inc2e-Organ mammary; Vector; poww.SoprRo, Site 1: sall; Site 2: Not! Cloned unidirectionally Primer: Gigo dr. Library constructed by Life Technologies. Investigators providing samples: Lother Hemiophausen/Priscilla Furth. Will Reference for Lrangenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
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BOMPT62TR BO_2_3 KB Brassica oleracea genomic clone BCMPT62, DNA
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Spermatophyra, Magnoliophyra; eudicotyledons; core eudicots;
Ronides: euroside II; Brassicales; Brassicacee; Brassica.
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DNA is from a doubled haploid provided by Tom Osborn.
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Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shorgun sequencing of Brassica oleracea
Unpublished (2001)
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                                                            /clone="IMAGE:5326811"
/clone lib="NCI CGAP_Mam#"
/tissue_type="tumor, gross tissue"
/dev stage="5 months"
/lab_host="DH108"
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    /strain="NMRI"
/db_xref="taxon:10090"
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/clone="BOMPT62"
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Class: sheared ends.
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Fax: 301-838-0208
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Spermatcophyta, Magnollophyta; endicoryledona; core endicocs;
Robinatcophyta, Magnollophyta; endicocs;
Robinatcophyta, Magnollophyta; endicocs;
Robinatcophyta, Magnollophyta; endicocs;
Town (LD., van Aken, S., Utterback, T. and Fraser, C.M.
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CDMA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Core distribution: McClane distribution information can be found through the I.M.A.G. Consortium/LLML at:
http://magel.lnl.gov. d. column: 12
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Mational Institutes of Health, Mammalian Gene Collection (MGC)
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Monobished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail nih.gov
Tissue Procurement: Lorbar Hennighausen Ph.D., Priscilla Purth
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/clone=1001KXT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-3523
Fax: 301-838-2028
Email: edcowneit.gr.org
DRA is from a doubled haploid provided by
Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 64;
tive 0; Mismatches
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Location/Qualifiers
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    BH571181.1 GI:17823020
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ALEG'972.1 GI:999902
GSS; genome survey sequence.
Tetradon ingroviridis.
SM Tetradon ingroviridis
Elizaryota, Metazoa; Chordata, Cruniata, Vertebrata; Buteleostomi;
Acanthomorpha: Acanthoperprisi, Felnostei; Buteleostei; Necteleostei;
Acanthomorpha: Acanthoperprisi Petradoni informes;
Tetradonidae; Tetradon.
B (Bose I to 1012)
S Roset-Crollius, M., Jaillon, O., Dusliva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fisames, C., Wincker, P., Brottier, P., Queiter, F.,
Human gene number estimate provide by genome wide analysis using
        uneausakr 1012 bp DNA linear GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
071E07 of library G from Tetraodon nigroviridis, genomic survey
AL26797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clonne-end sequencing project of the Tetraodon nigroviridis genome. For more information, pluase take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1012)
Roses-Crollius.H., Jaillon,O., Dusilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,M., Bernot,A. and
Waissenbach,J.
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Query Match 9.9; Score 18; DB 17; Length 1012; Best Local Similarity 100.04; Pred, No. 67; Matches 18; Conservative 0; Mismatches 0; Indels (

Search completed: June 9, 2003, 12:46:04 Job time : 1117 secs

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